

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2003, 10:33:36 ; Search time 73 Seconds

(without alignments)
1084.258 Million cell updates/sec

Title: US-10-080-233-2

Perfect score: 3189

Sequence: 1 MLFRSMQLAAAGSLTSGVLG.....AQEPYRDEILEDGIEE 594

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Minimum number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A: Geneseq.101002:*

1:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
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16:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
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19:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3189	100.0	594	20	Stachybotrys chart
2	3189	100.0	594	20	Stachybotrys pheno
3	3189	100.0	594	21	Stachybotrys chart
4	3189	100.0	594	21	Stachybotrys chart
5	3189	100.0	594	23	Stachybotrys phenol
6	1954.5	61.3	627	21	Biopolaris spicifer
7	1954.5	61.3	627	21	Biopolaris spicifer
8	1954.5	61.3	627	23	Biopolaris spicifer
9	1929.5	60.5	627	21	Curvularia pallesc
10	1929.5	60.5	627	21	Curvularia pallesc

11	1929.5	60.5	627	23	AA018212	C pallescens pheno
12	1735.5	54.4	583	23	AA097312	Phenol oxidising e
13	1731.5	54.3	583	23	AA097316	Phenol oxidising e
14	1731.5	54.3	583	23	AA097318	Phenol oxidising e
15	1731.5	54.3	583	23	AA097318	Phenol oxidising e
16	1731.5	54.3	583	23	AA097318	Phenol oxidising e
17	1730.5	54.3	583	23	AA097321	Phenol oxidising e
18	1730.5	54.3	583	23	AA097324	Phenol oxidising e
19	1730.5	54.3	583	23	AA097323	Phenol oxidising e
20	1730.5	54.3	583	23	AA097323	Phenol oxidising e
21	1730.5	54.3	583	23	AA097323	Phenol oxidising e
22	1730.5	54.3	583	23	AA097329	Phenol oxidising e
23	1729.5	54.2	583	23	AA097329	Phenol oxidising e
24	1729.5	54.2	583	23	AA097334	Phenol oxidising e
25	1729.5	54.2	583	23	AA097336	Phenol oxidising e
26	1729.5	54.2	583	23	AA097336	Phenol oxidising e
27	1729.5	54.2	583	23	AA097336	Phenol oxidising e
28	1729.5	54.2	583	23	AA097336	Phenol oxidising e
29	1729.5	54.2	583	23	AA097336	Phenol oxidising e
30	1728.5	54.2	583	23	AA097333	Phenol oxidising e
31	1728.5	54.2	583	23	AA097337	Phenol oxidising e
32	1728.5	54.2	583	23	AA097338	Phenol oxidising e
33	1728.5	54.2	583	23	AA097356	Phenol oxidising e
34	1728.5	54.2	583	23	AA097356	Phenol oxidising e
35	1728.5	54.2	583	23	AA097356	Phenol oxidising e
36	1728.5	54.2	583	23	AA097356	Phenol oxidising e
37	1728.5	54.2	583	23	AA097356	Phenol oxidising e
38	1728.5	54.2	583	23	AA097356	Phenol oxidising e
39	1728.5	54.2	583	23	AA097356	Phenol oxidising e
40	1728.5	54.2	583	23	AA097356	Phenol oxidising e
41	1727.5	54.2	583	23	AA097326	Phenol oxidising e
42	1727.5	54.2	583	23	AA097326	Phenol oxidising e
43	1727.5	54.2	583	23	AA097335	Phenol oxidising e
44	1727.5	54.2	583	23	AA097335	Phenol oxidising e
45	1727.5	54.2	583	23	AA097335	Phenol oxidising e

ALIGNMENTS

RESULT 1
AA045222 standard; Protein: 594 AA.
ID AA045222: standard; Protein: 594 AA.
AC AA045222: standard; Protein: 594 AA.
DE 05-JAN-2000 (first entry)
XX
XX Stachybotrys chartarum phenol oxidising enzyme.
XX Stachybotrys chartarum phenol oxidising enzyme; colour: dye;
XX detergent; anti-dye transfer; stain removal; bleaching.
XX
XX Stachybotrys chartarum.
XX
XX MO9949010-A2.
XX
XX 30-SEP-1999.
XX
XX 23-MAR-1999; 99WO-EP02042.
XX
XX 24-MAR-1998; 98US-0046969.
XX
XX 22-DEC-1998; 98US-0218702.
XX
XX (UNITL) UNILEVER NV.
XX (UNITL) UNILEVER PLC.
XX
XX Convents D, Amory A, Wang H, Dhasee P, Lambrechts-Rongvaux A;
XX Wang C.
XX WPI, 1999-601211/51.
XX N-PSDB; AA25727.
XX

PT Detergent composition containing phenol oxidase from Stachybotrys, used
 to bleach stains and prevent dye transfer
 PS Claim 16; Fig 5; 56pp; English.

CC The present invention describes a detergent composition containing a
 purified phenol oxidizing enzyme derived from Stachybotrys. The present
 CC sequence represents Stachybotrys chartarum phenol oxidizing enzyme. The
 CC enzyme can be used to modify the colour of dyes and other coloured
 CC compounds (e.g. for use in pulp and paper bleaching also for removing
 CC stains, e.g. food, tea, blood etc., from fabrics) and for preventing dye
 CC transfer during fabric washing.

XX Sequence 594 AA;

Query Match 100.0%; Score 3189; DB 20; Length 594;
 Best Local Similarity 100.0%; Pred. No. 2,9e-299;
 Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLFNSWQLAASGLISGLVIGIPMDTGSHPTEAVDEPVKTEVFADSLAAGDDWESPYP 60
 1 MLFNSWQLAASGLISGLVIGIPMDTGSHPTEAVDEPVKTEVFADSLAAGDDWESPYP 60
 1 MLFNSWQLAASGLISGLVIGIPMDTGSHPTEAVDEPVKTEVFADSLAAGDDWESPYP 60
 61 NLTYRNALPIPVKOPKMITNPVTKDIWYETIEIKFPQOIRYPTLRPATLVGDGMS 120
 61 NLTYRNALPIPVKOPKMITNPVTKDIWYETIEIKFPQOIRYPTLRPATLVGDGMS 120
 121 GPTFVVRGTEVAFINNATVENSVHLHGSRSRAPFGMAEDVTFPEYKDYEPNQS 180
 121 GPTFVVRGTEVAFINNATVENSVHLHGSRSRAPFGMAEDVTFPEYKDYEPNQS 180
 121 GPTFVVRGTEVAFINNATVENSVHLHGSRSRAPFGMAEDVTFPEYKDYEPNQS 180
 181 ARLLMYHDHAFMKTAEENAYFCGACAYIINDEAEDALGPSGGEFDIPILITAKYYNADG 240
 181 ARLLMYHDHAFMKTAEENAYFCGACAYIINDEAEDALGPSGGEFDIPILITAKYYNADG 240
 241 TLRSFEGDODLMGVHVNQOPMPELVNORPKYRFRFLNAVSAMLLYLVRTSSPNVR 300
 241 TLRSFEGDODLMGVHVNQOPMPELVNORPKYRFRFLNAVSAMLLYLVRTSSPNVR 300
 301 IPFOVIASDAGILQAPVOTSNLYLAVEREYIIDFTNFAGOTLDRNVAETNDVGDEDE 360
 301 IPFOVIASDAGILQAPVOTSNLYLAVEREYIIDFTNFAGOTLDRNVAETNDVGDEDE 360
 361 YARLLEVMRFVYSSGTEVDNSQVSTLRDVPFPKKEGSPADKHFEKRSNGHYLLINDYGF 420
 361 YARLLEVMRFVYSSGTEVDNSQVSTLRDVPFPKKEGSPADKHFEKRSNGHYLLINDYGF 420
 421 ADVNERVLAKPELGVEWELENSGSGSHPHVHLVDFTKLKRTGGGQVMPYESAGLK 480
 421 ADVNERVLAKPELGVEWELENSGSGSHPHVHLVDFTKLKRTGGGQVMPYESAGLK 480
 481 DVVNLGRGETLTIEAHYOPTGAYMMHCHNLIHEDNDMAAFVNTYAMEEKGYLQEDFEDP 540
 481 DVVNLGRGETLTIEAHYOPTGAYMMHCHNLIHEDNDMAAFVNTYAMEEKGYLQEDFEDP 540
 541 MNPWRAPVYRNDFHARAGNFSASITARVOELAEOPYRNLDLIEDLGIEE 594
 541 MNPWRAPVYRNDFHARAGNFSASITARVOELAEOPYRNLDLIEDLGIEE 594

RESULT 2
 AAY39992
 ID AAY39992 standard; Protein; 594 AA.

XX AAY39992;
 XX 16-DEC-1999 (first entry)
 XX Stachybotrys phenol oxidase protein sequence.
 XX Phenol oxidase; enzyme; coloured compound; dye transfer prevention;
 KW fabric washing; stain bleaching; anti-dye transfer; detergent.
 XX

OS Stachybotrys chartarum.

XX WO9949020-A2.

XX 30-SEP-1999.

XX 23-MAR-1999; 99WO-US06327.

XX 22-MAR-1998; 98US-0046969.

XX 22-DEC-1998; 98US-0218702.

XX 22-MAR-1999; 99US-0273957.

XX (GENV) GENENCOR INT INC.

XX Amory A, Wang H, Dhase P, Lambrechts-Rongvaux A, Wang C;

XX WPT: 1999-591086/50.

XX N-PSDB: AA227601, AA227602.

XX Novel enzyme for modifying coloured compounds used to prevent
 PT dye-transfer.

CC Claim 16; Fig 5; 64pp; English.
 CC This sequence is the Stachybotrys chartarum phenol oxidase enzyme
 CC of the invention. The invention is used to modify a coloured compound and
 CC prevent dye transfer during fabric washing, or for stain bleaching or
 CC anti-dye transfer. It is useful in the detergent, paper and pulp, textile
 CC and food industries.

XX Sequence 594 AA;

Query Match 100.0%; Score 3189; DB 20; Length 594;
 Best Local Similarity 100.0%; Pred. No. 2,9e-299;
 Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLFNSWQLAASGLISGLVIGIPMDTGSHPTEAVDEPVKTEVFADSLAAGDDWESPYP 60
 1 MLFNSWQLAASGLISGLVIGIPMDTGSHPTEAVDEPVKTEVFADSLAAGDDWESPYP 60
 1 MLFNSWQLAASGLISGLVIGIPMDTGSHPTEAVDEPVKTEVFADSLAAGDDWESPYP 60
 61 NLTYRNALPIPVKOPKMITNPVTKDIWYETIEIKFPQOIRYPTLRPATLVGDGMS 120
 61 NLTYRNALPIPVKOPKMITNPVTKDIWYETIEIKFPQOIRYPTLRPATLVGDGMS 120
 121 GPTFVVRGTEVAFINNATVENSVHLHGSRSRAPFGMAEDVTFPEYKDYEPNQS 180
 121 GPTFVVRGTEVAFINNATVENSVHLHGSRSRAPFGMAEDVTFPEYKDYEPNQS 180
 121 GPTFVVRGTEVAFINNATVENSVHLHGSRSRAPFGMAEDVTFPEYKDYEPNQS 180
 181 ARLLMYHDHAFMKTAEENAYFCGACAYIINDEAEDALGPSGGEFDIPILITAKYYNADG 240
 181 ARLLMYHDHAFMKTAEENAYFCGACAYIINDEAEDALGPSGGEFDIPILITAKYYNADG 240
 241 TLRSFEGDODLMGVHVNQOPMPELVNORPKYRFRFLNAVSAMLLYLVRTSSPNVR 300
 241 TLRSFEGDODLMGVHVNQOPMPELVNORPKYRFRFLNAVSAMLLYLVRTSSPNVR 300
 301 IPFOVIASDAGILQAPVOTSNLYLAVEREYIIDFTNFAGOTLDRNVAETNDVGDEDE 360
 301 IPFOVIASDAGILQAPVOTSNLYLAVEREYIIDFTNFAGOTLDRNVAETNDVGDEDE 360
 361 YARLLEVMRFVYSSGTEVDNSQVSTLRDVPFPKKEGSPADKHFEKRSNGHYLLINDYGF 420
 361 YARLLEVMRFVYSSGTEVDNSQVSTLRDVPFPKKEGSPADKHFEKRSNGHYLLINDYGF 420
 421 ADVNERVLAKPELGVEWELENSGSGSHPHVHLVDFTKLKRTGGGQVMPYESAGLK 480
 421 ADVNERVLAKPELGVEWELENSGSGSHPHVHLVDFTKLKRTGGGQVMPYESAGLK 480
 481 DVVNLGRGETLTIEAHYOPTGAYMMHCHNLIHEDNDMAAFVNTYAMEEKGYLQEDFEDP 540
 481 DVVNLGRGETLTIEAHYOPTGAYMMHCHNLIHEDNDMAAFVNTYAMEEKGYLQEDFEDP 540
 541 MNPWRAPVYRNDFHARAGNFSASITARVOELAEOPYRNLDLIEDLGIEE 594
 541 MNPWRAPVYRNDFHARAGNFSASITARVOELAEOPYRNLDLIEDLGIEE 594

Db 541 MNPKRAVPYNRNDFHARAGNFSAESITARVOELAEDEPYNRLEIDEDGIEE 594

RESULT 3
AAV95537
ID AAV95537 standard; Protein: 594 AA.
XX
AC AAV95537;
XX
DT 10-OCT-2000 (first entry)
XX
DE Stachybotrys chartarum phenol oxidizing enzyme.
XX
KM Phenol oxidizing enzyme; detergent; bleaching.
XX
OS Stachybotrys chartarum.
XX
NM WO200039306-A2.
XX
PI 06-JUL-2000.
XX
PF 20-DEC-1999; 99WO-EPI0287.
XX
PR 23-DEC-1998; 98US-0220871.
XX
PR 23-JUN-1999; 99US-0338723.
XX
PA (UNITL) UNILEVER NV.
PA (UNITL) UNILEVER PLC.
PA (HIND-) HINDUSTAN LEVER LTD.
XX
PI Bodle EA, Van Der Velden S, De Vries CH, Wang H;
XX
DR WPI: 2000-514528/46.
XX
DR N-PSDB; AAA50018, AAA50019.
XX
PT Detergent composition comprising novel phenol oxidizing enzyme obtained
PT from fungus or bacteria, useful for pulp and paper bleaching, bleaching
PT color of stains on fabric and for anti-dye redeposition
XX
PS Claim 2; Fig 5A-B; 45pp; English.
XX
XX The present sequence is that of a phenol oxidizing enzyme of
XX Stachybotrys chartarum MUCI 38898. A claimed detergent composition
XX comprises a phenol oxidizing enzyme having at least 60% identity to
XX the present sequence, and preferably obtained from a bacterium,
XX yeast or non-Stachybotrys fungus, especially Bipolaris spicifera,
XX Curvularia pallescens or Amersporium atrum (see AAV95538-40). The
XX phenol oxidizing enzyme is capable of modifying the colour
XX associated with dyes or coloured compounds, and can be used for
XX pulp and paper bleaching, for bleaching the colour of stains on
XX fabric and for anti-dye transfer in detergent and textile
XX applications. It may also be capable of modifying the colour in
XX the absence or presence of an enhancer. Expression vectors and
XX host cells comprising a nucleic acid encoding a phenol oxidizing
XX enzyme, methods for producing the phenol oxidizing enzyme, and
XX methods for constructing expression hosts are provided.
XX
SQ Sequence 594 AA;
XX
Query Match 100.0%; Score 3189; DB 21; Length 594;
Best Local Similarity 100.0%; Pred. No. 2,9e-299;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLEKSNQLAASGLSGVIGIPMDTGSHPLEAVDPKKTVEFADSLIAAGDDWESPPY 60
QY 1 MLEKSNQLAASGLSGVIGIPMDTGSHPLEAVDPKKTVEFADSLIAAGDDWESPPY 60
QY 1 MLEKSNQLAASGLSGVIGIPMDTGSHPLEAVDPKKTVEFADSLIAAGDDWESPPY 60
Db 1 MLEKSNQLAASGLSGVIGIPMDTGSHPLEAVDPKKTVEFADSLIAAGDDWESPPY 60
QY 1 MLEKSNQLAASGLSGVIGIPMDTGSHPLEAVDPKKTVEFADSLIAAGDDWESPPY 120
QY 1 MLEKSNQLAASGLSGVIGIPMDTGSHPLEAVDPKKTVEFADSLIAAGDDWESPPY 120
Db 61 NLLYRNALPPIPKOPKMITTNPVTGKDIYVEIETIKPQORITPTLTPATLVGYGOSMP 120
QY 61 NLLYRNALPPIPKOPKMITTNPVTGKDIYVEIETIKPQORITPTLTPATLVGYGOSMP 120
Db 61 NLLYRNALPPIPKOPKMITTNPVTGKDIYVEIETIKPQORITPTLTPATLVGYGOSMP 120
QY 61 NLLYRNALPPIPKOPKMITTNPVTGKDIYVEIETIKPQORITPTLTPATLVGYGOSMP 180
QY 121 GPTFNVRGTETVVRFINNATVENSVLHSGSPSRAPFDGWAEDVTFEGEYKDYFPYQS 180

Db 121 GPTFNVRGTETVVRFINNATVENSVLHSGSPSRAPFDGWAEDVTFEGEYKDYFPYQS 180

QY 181 ARLLMYHDHAFMKTAENAFYGOAGAYIINDEADALGPSGCEFDIPLITAKYVADG 240
Db 181 ARLLMYHDHAFMKTAENAFYGOAGAYIINDEADALGPSGCEFDIPLITAKYVADG 240
QY 241 TLNSTEGEDDLMGDVILHVGQPPFLNVOCPKRYRFRFLNAAVSRALLLYVPTSSPNVR 300
Db 241 TLNSTEGEDDLMGDVILHVGQPPFLNVOCPKRYRFRFLNAAVSRALLLYVPTSSPNVR 300
QY 301 IPFOVIASDAGLLQAPVQTSNLYLAVEREYIITFTNFAQOTLDLRNVAETNDVGEDE 360
Db 301 IPFOVIASDAGLLQAPVQTSNLYLAVEREYIITFTNFAQOTLDLRNVAETNDVGEDE 360
QY 361 YARTLEVMRVYSSGTYEDNSQVSTLRDVPFPKKGPAKHKFRSNGHYLINDVGF 420
Db 361 YARTLEVMRVYSSGTYEDNSQVSTLRDVPFPKKGPAKHKFRSNGHYLINDVGF 420
QY 421 ADVNERVLAKPELGTEVWELENSSGGMSHPVHILVDKFKRTGGRGOVMPESAGLK 480
Db 421 ADVNERVLAKPELGTEVWELENSSGGMSHPVHILVDKFKRTGGRGOVMPESAGLK 480
QY 481 DVMWLGRETLLTEAHYQPTGAYMMCHNLIEDNDMAVFNTYAMEEKGYLOEDFEDP 540
Db 481 DVMWLGRETLLTEAHYQPTGAYMMCHNLIEDNDMAVFNTYAMEEKGYLOEDFEDP 540
QY 541 MNPKRAVPYNRNDFHARAGNFSAESITARVOELAEDEPYNRLEIDEDGIEE 594
Db 541 MNPKRAVPYNRNDFHARAGNFSAESITARVOELAEDEPYNRLEIDEDGIEE 594

RESULT 4
AAV96761
ID AAV96761 standard; Protein: 594 AA.
XX
AC AAV96761;
XX
DT 09-OCT-2000 (first entry)
XX
XX Stachybotrys chartarum phenol oxidizing enzyme.
XX
DE Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;
XX KM pulp; paper bleaching.
XX
OS Stachybotrys chartarum.
XX
PN WO200037654-A2.
XX
PD 29-JUN-2000.
XX
PF 20-DEC-1999; 99WO-US31009.
XX
PR 23-DEC-1998; 98US-0220871.
XX
PR 23-JUN-1999; 99US-0338723.
XX
PA (GENV) GENENCOR INT INC.
XX
PI Wang H, Bodle EA;
XX
DR WPI: 2000-452191/39.
XX
DR N-PSDB; AAA51313, AAA51314.
XX
PT New phenol oxidizing enzyme for modifying colors associated with dyes
PT or colored compounds, is obtained from fungus and is encoded by a
PT nucleic acid comprising a specific nucleotide sequence
XX
PS Claim 1; Fig 5A-B; 45pp; English.
XX
XX This is the sequence of Stachybotrys chartarum phenol oxidizing enzyme.
XX Phenol oxidizing enzymes encoded by nucleic acid sequences which
XX hybridize to the coding DNA are claimed, as long as the enzyme is capable
XX of modifying the colour associated with dyes or coloured compounds. The

CC enzymes are useful in detergent compositions and for modifying colors
CC associated with dyes or colored compounds which occur in stains in a
CC sample. The enzymes are also useful for pulp and paper bleaching,
CC anti-dye transfer in detergent and other textile applications.

XX
SQ Sequence 594 AA;

Query Match 100.0%; Score 3189; DB 21; Length 594;
Best Local Similarity 100.0%; Pred. No. 2,9e-299;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MLEKSMQLAASGLISGLVIGIPMDTGSHPHIEAVDEVEKTEVFADSLAAAGDDMESPPY 60
DB 1 MLEKSMQLAASGLISGLVIGIPMDTGSHPHIEAVDEVEKTEVFADSLAAAGDDMESPPY 60
OY 61 NLLYNALPIPPVKOPKMIITNPYTKDIWYEIEIKFPQOIRYPTLRPATLVGDGMS 120
DB 61 NLLYNALPIPPVKOPKMIITNPYTKDIWYEIEIKFPQOIRYPTLRPATLVGDGMS 120
OY 121 GPTFNVPRTETVVFINNATVENSVHLHGSFSRAPFDGMADVTFFPEYKDYEPNYS 180
DB 121 GPTFNVPRTETVVFINNATVENSVHLHGSFSRAPFDGMADVTFFPEYKDYEPNYS 180
OY 121 GPTFNVPRTETVVFINNATVENSVHLHGSFSRAPFDGMADVTFFPEYKDYEPNYS 180
DB 121 GPTFNVPRTETVVFINNATVENSVHLHGSFSRAPFDGMADVTFFPEYKDYEPNYS 180
OY 181 ARLLMYHDAEFKTAENAYFCGAGAYIINDEAEDALGPSYGEEDIPILITAKYNNADG 240
DB 181 ARLLMYHDAEFKTAENAYFCGAGAYIINDEAEDALGPSYGEEDIPILITAKYNNADG 240
OY 241 TLRTSGEDODLMDGVHIVNGQPMPEFLNVPKRYFRFLNAVSAMLLYLVRTSSPNVR 300
DB 241 TLRTSGEDODLMDGVHIVNGQPMPEFLNVPKRYFRFLNAVSAMLLYLVRTSSPNVR 300
OY 301 IPFOVIASDAGLLQAPVOTSNLYLVAERYEIIIDFTNFAQTLDLRNVAETNDVGDE 360
DB 301 IPFOVIASDAGLLQAPVOTSNLYLVAERYEIIIDFTNFAQTLDLRNVAETNDVGDE 360
OY 361 YARLLEVMRFVYSSGTVEDNSQVSTLSDVPPPKKEGPADKHFEKFSNGHYLLINDVGF 420
DB 361 YARLLEVMRFVYSSGTVEDNSQVSTLSDVPPPKKEGPADKHFEKFSNGHYLLINDVGF 420
OY 421 ADVNERVLAKPELGVEVWELENSSGSHVPHILVDFKILKRTGGRGVMPYESSAGLK 480
DB 421 ADVNERVLAKPELGVEVWELENSSGSHVPHILVDFKILKRTGGRGVMPYESSAGLK 480
OY 481 DVVWLGREGTELTIEAHYOPWTGAYVMHCHNLIHEDNDMAAFVNTVAMEKGYLQEDFDP 540
DB 481 DVVWLGREGTELTIEAHYOPWTGAYVMHCHNLIHEDNDMAAFVNTVAMEKGYLQEDFDP 540
OY 541 MNPKRAVPYRNDFHARAGNFSASITARVOELAEOPRYNRDLDEILDGIEE 594
DB 541 MNPKRAVPYRNDFHARAGNFSASITARVOELAEOPRYNRDLDEILDGIEE 594
```

RESULT 5
AA018210 standard; Protein; 594 AA.

AC AA018210;
DT 13-SEP-2002 (first entry)
DE S charatarum phenol oxidizing enzyme.
KW Phenol oxidizing enzyme; fungus; redox reaction; detergent;
KW paper industry; pulp industry; textile; food industry.

XX Stachybotrys charatarum.

XX US6399329-B1.

XX 04-JUN-2002.

XX 21-DEC-1999; 99US-0468578.

PR 12-DEC-1996; 98US-0220871.
PR 23-JUN-1999; 99US-0338723.
XX
XX (GENEW) GENENCOR INT INC.

PI Wang H, Bodie EA;
XX
XX WPI; 2002-498835/53.
DR N-PSDB; AAL47582, AAL47584.

PT New polynucleotides encoding phenol oxidizing enzymes, useful for
PT preventing the transfer of dyes in solution from one textile to another
PT during detergent washing -

PS Example 5; Fig 4; 37pp; English.

CC The present invention provides the protein and coding sequences of phenol
CC oxidizing enzymes from Stachybotrys charatarum, Bipolaris splicifera and
CC Curvularia pallescens. These enzymes are useful in the textiles, paper,
CC pulp, detergent and food industries. In particular they are useful for
CC preventing the transfer of dyes in solution from one textile to another
CC during detergent washing (dye transfer inhibition). The present sequence
CC is the S. charatarum phenol oxidizing enzyme.

XX Sequence 594 AA;

Query Match 100.0%; Score 3189; DB 23; Length 594;
Best Local Similarity 100.0%; Pred. No. 2,9e-299;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MLEKSMQLAASGLISGLVIGIPMDTGSHPHIEAVDEVEKTEVFADSLAAAGDDMESPPY 60
DB 1 MLEKSMQLAASGLISGLVIGIPMDTGSHPHIEAVDEVEKTEVFADSLAAAGDDMESPPY 60
OY 61 NLLYNALPIPPVKOPKMIITNPYTKDIWYEIEIKFPQOIRYPTLRPATLVGDGMS 120
DB 61 NLLYNALPIPPVKOPKMIITNPYTKDIWYEIEIKFPQOIRYPTLRPATLVGDGMS 120
OY 121 GPTFNVPRTETVVFINNATVENSVHLHGSFSRAPFDGMADVTFFPEYKDYEPNYS 180
DB 121 GPTFNVPRTETVVFINNATVENSVHLHGSFSRAPFDGMADVTFFPEYKDYEPNYS 180
OY 181 ARLLMYHDAEFKTAENAYFCGAGAYIINDEAEDALGPSYGEEDIPILITAKYNNADG 240
DB 181 ARLLMYHDAEFKTAENAYFCGAGAYIINDEAEDALGPSYGEEDIPILITAKYNNADG 240
OY 241 TLRTSGEDODLMDGVHIVNGQPMPEFLNVPKRYFRFLNAVSAMLLYLVRTSSPNVR 300
DB 241 TLRTSGEDODLMDGVHIVNGQPMPEFLNVPKRYFRFLNAVSAMLLYLVRTSSPNVR 300
OY 301 IPFOVIASDAGLLQAPVOTSNLYLVAERYEIIIDFTNFAQTLDLRNVAETNDVGDE 360
DB 301 IPFOVIASDAGLLQAPVOTSNLYLVAERYEIIIDFTNFAQTLDLRNVAETNDVGDE 360
OY 361 YARLLEVMRFVYSSGTVEDNSQVSTLSDVPPPKKEGPADKHFEKFSNGHYLLINDVGF 420
DB 361 YARLLEVMRFVYSSGTVEDNSQVSTLSDVPPPKKEGPADKHFEKFSNGHYLLINDVGF 420
OY 421 ADVNERVLAKPELGVEVWELENSSGSHVPHILVDFKILKRTGGRGVMPYESSAGLK 480
DB 421 ADVNERVLAKPELGVEVWELENSSGSHVPHILVDFKILKRTGGRGVMPYESSAGLK 480
OY 481 DVVWLGREGTELTIEAHYOPWTGAYVMHCHNLIHEDNDMAAFVNTVAMEKGYLQEDFDP 540
DB 481 DVVWLGREGTELTIEAHYOPWTGAYVMHCHNLIHEDNDMAAFVNTVAMEKGYLQEDFDP 540
OY 541 MNPKRAVPYRNDFHARAGNFSASITARVOELAEOPRYNRDLDEILDGIEE 594
DB 541 MNPKRAVPYRNDFHARAGNFSASITARVOELAEOPRYNRDLDEILDGIEE 594
```

RESULT 6
AAV95538


```

ID  AAY95538 standard; Protein; 627 AA.
XX
AC  AAY95538;
XX
DT  10-OCT-2000 (first entry)
XX
DE  Bipolaris spicifera phenol oxidizing enzyme.
XX
KM  Phenol oxidizing enzyme; detergent; bleaching.
XX
OS  Bipolaris spicifera.
XX
PN  MO200039306-A2.
XX
PD  06-JUL-2000.
XX
PF  20-DEC-1999; 99MO-EP10287.
XX
PR  23-DEC-1998; 98US-0220871.
XX
PS  23-JUN-1999; 99US-0338723.
XX
PA  (UNITL ) UNILEVER NV.
XX  (UNITL ) UNILEVER PLC.
XX  (HIND-) HINDUSTAN LEVER LTD.
XX
PI  Bodie EA, Van Der Velden S, De Vries CH, Wang H;
XX
DR  WPI; 2000-514528/46.
XX  N-PSDB; AAA50020.
XX
PT  Detergent composition comprising novel phenol oxidizing enzyme obtained
PT  from fungus or bacteria, useful for pulp and paper bleaching, bleaching
PT  color of stains on fabric and for anti-dye redeposition
XX
PS  Claim 8; Fig 3; 45pp; English.
XX
XX
XX  The present sequence is that of the Bipolaris spicifera
XX  phenol oxidizing enzyme. The invention relates to detergent
XX  compositions comprising novel phenol oxidizing enzymes that have at
XX  least 60% identity with the phenol oxidizing enzyme of Stachybotrys
XX  chartarum (see AAY95537), and which are obtained from a bacterium,
XX  yeast or non-Stachybotrys fungus, especially B. spicifera,
XX  Curvularia pallescens (see AAY95539) and Amerosporium atrum (see
XX  AAY95540). The phenol oxidizing enzyme is capable of modifying the
XX  colour associated with dyes or coloured compounds, and can be used
XX  for pulp and paper bleaching, for bleaching the colour of stains on
XX  fabric and for anti-dye transfer in detergent and textile
XX  applications. It may also be capable of modifying the colour in
XX  the absence or presence of an enhancer. Expression vectors and
XX  host cells comprising a nucleic acid encoding a phenol oxidizing
XX  enzyme, methods for producing the phenol oxidizing enzyme, and
XX  methods for constructing expression hosts are provided.
XX
SQ  Sequence 627 AA:
XX
Query Match 61.3%; Score 1954.5; DB 21; Length 627;
Best Local Similarity 61.1%; Pred. NO. 1e-179;
Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8;
XX
OY  2 LKSMQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTGFADSLAAGDD----- 53
DB  6 LKSAQLQVLS---IAKGIYCVAL--SERPAKFVDNPFDEKKA--LASIYEDDPADVVMNL 58
OY  54 -PMESPPYLLRLNALPIPVKQPKMTITNPYTGKIIYWEIEIKFQORITPTLPAPL 112
DB  59 KMQSPSEYPLIRQPLIPPAKEPNK-LINPVYTNKIKWIEYIKFTQOYVPSLPAPL 117
OY  113 VGYDGSPPGTFFNVPGTETVVFRTINATVENSVHLGSPSRAPFGMAEDVTFPEYRD 172
DB  118 VGYDGSPPGTITIVRGTAVYRFINOGRESSIHHLGSPSRAPFGMADDMKGEYRD 177
OY  173 YTFPNQASRLIMYHDHAPMKTAENAVFGQAGAYIINDAEALGLPSGYGEFDIPLILT 232
DB  173 YTFPNQASRLIMYHDHAPMKTAENAVFGQAGAYIINDAEALGLPSGYGEFDIPLILT 232

```

```

DB  178 YYYPNNOAARFLMYHDHAPMTAENAVFGQAGAYLITDPEDALGLPSGYGYDIPLVLS 237
OY  233 AKTYNADGTRRSTEGEDDLMGVYHNGQPMFPLVNOPRKRYFRFLNAAVSRAMLLYLV 292
DB  238 SKYYNADGTRKTSVGBDKSYWGDIIHNGQPMFPLVNEPRKRYFRFLNAAVSRMFLYLV 297
OY  293 RTSSPNVRIPEFOYIASDAGLLQAPVOTSNLYLVAERYEYIIIDFTNPAGOTLDRVAET 352
DB  298 KQDNTATRLPFOYIASDAGLLTTPVOTSDMTYVAAAREYELVFPPAPAGOTLDRPAPA 357
OY  353 NDVDEDEKARTLEVAFVSVSGTVDNSQVPSLTLDVPPPKRKEPADKHFEPERSNGH 412
DB  358 NGIGTDDQVANKTKVRFHYSQOTVVDNSVPEQLSQIQPDAKT-DIDHFFPHRTNGE 416
OY  413 YLINDVGFADVNRVLAKEPLGTVEYWELENSSGSHPHHILNDFKILKRGGQ-- 470
DB  417 WRINGIGFADVENRVLAKVPRGIVELMELENSGSGSHPIHVLVDFRVARVYDGTGRC 476
OY  471 VMPYESAGLKDVYVLGRGETLTTEAHYOPMTGAYMMHCHNLTHEDDNMAVFPVPTAMEEK 530
DB  477 VMPYEAAGLKDVYVLGRHETVLEAHAPMDGVYMFHCHNLTHEDDNMAAFVYTKQNF 536
OY  531 GYLQ-EDFEDPMNPKRAVFPYNNDFHARAGNSAESITARVQELAEQEPYRLDEILED 589
DB  537 GYNETDHFDPEDPRMSARFPTAGDLTARSGIFSESIRARVVELLEQYSELAQVTA 596
OY  590 L 590
DB  597 L 597
XX
XX  RESULT 7
XX  AAY96762
XX  ID  AAY96762 standard; Protein; 627 AA.
XX
XX  AC  AAY96762;
XX
XX  DT  09-OCT-2000 (first entry)
XX
XX  DE  Bipolaris spicifera phenol oxidizing enzyme.
XX
XX  KM  Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;
XX  pulp; paper bleaching.
XX
XX  OS  Bipolaris spicifera.
XX
XX  PN  MO200037654-A2.
XX
XX  PD  29-JUN-2000.
XX
XX  PF  20-DEC-1999; 99MO-US31009.
XX
XX  PR  23-DEC-1998; 98US-0220871.
XX  23-JUN-1999; 99US-0338723.
XX
XX  PA  (GENEV ) GENENCOR INT INC.
XX
XX  PI  Wang H, Bodie EA;
XX
XX  PT  WPI; 2000-452191/39.
XX  N-PSDB; AAA51315.
XX
XX  PS  New phenol oxidizing enzyme for modifying colors associated with dyes
XX  or colored compounds, is obtained from fungus and is encoded by a
XX  nucleic acid comprising a specific nucleotide sequence
XX
XX  Claim 8; Fig 3; 45pp; English.
XX
XX  This sequence is the Bipolaris spicifera phenol oxidizing enzyme.
XX  Phenol oxidizing enzymes encoded by nucleic acid sequences which
XX  hybridize to the Stachybotrys chartarum DNA (AA51313) are claimed, as
XX  long as the enzyme is capable of modifying the colour associated with
XX  dyes or coloured compounds. The enzymes are useful in detergent

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CC compositions and for modifying colors associated with dyes or coloured
CC compounds which occur in stains in a sample. The enzymes are also useful
CC for pulp and paper bleaching, anti-dye transfer in detergent and other
CC textile applications.

XX Sequence 627 AA;

Query Match 61.3%; Score 1954.5; DB 21; Length 627;
Best Local Similarity 61.1%; Pred. No. 1e-179;
Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8;

QY 2 LFKSMQLAAAGSLGVLGIPMDGSHPIEAVDEPVKTEVADSLAAAGD----- 53
DB 6 LFSALQLVLS---LAKGITGVAL--SERPAKVDNTPDEKAA--LASTVEDDPADVNM 58
QY 54 -DMESPYNLLRYNALPIPVKOPKMITNPVTKDVIYVEIEIKPFOQRIYPTLRPATL 112
DB 59 KDMQSPERPLIFRQPLPIPAKEPNK-LTNVTKKEIWEYELVIAKPFQGYPSLRPARL 117

113 VGYDGMSPGPTFNPRGTEYVVRFLNNATVENSVHLGSPSRAPFDGMAEDVTPPEGYKD 172
118 VGYGISPGPTIIVPRGTEAVVRFLNODRESSIHLGSPSRAPFDGMAEDVTPPEGYKD 177
QY 173 YYPFNQOSARLLMWDHAFMKTAENAYFGAGATYINDAEDALGSPGYGEFDPIPLLT 232
DB 178 YYPFNQOSARLLMWDHAFMKTAENAYFGAGATYINDAEDALGSPGYGEFDPIPLLT 237

QY 233 AKYNNADGTLRSTEGEDQDLMDVYIHVNGQWPPELVNQPRKRYRFRFLNAAVSRAVLTYLV 292
DB 238 SKYYNADGTLRSTEGEDQDLMDVYIHVNGQWPPELVNQPRKRYRFRFLNAAVSRAVLTYLV 297
QY 293 RTSSPNVRIIPROVIAASDAGLLQAPVQTSNLYLAVEREYIITFTNAGQTLDIRNAET 352
DB 298 KQDNTATRLPPOVIAASDAGLLTHHPVQTSNLYLAVEREYIITFTNAGQTLDIRNAET 357

QY 353 NDVDEDEYARTLEVMRNVVSSGTEVENSQVPTLRDVPFPKKEGPAKDKFKPERSNGH 412
DB 358 NGIGTDDYANTDKVMREHVSQTVVDSVVPBLSQIOPADKT-DIDHFRHRTNGE 416
QY 413 YLINDVGADVNERVLAKPELGTEVEWELNENSSGWSHPVHILHVEFKILRTGSGO-- 470
DB 417 WRINGIGADVNERVLAKPELGTEVEWELNENSSGWSHPVHILHVEFKILRTGSGO-- 476

QY 471 VMPYESAGLKDVVNLGREGTLLTAHQPWTGAYMMCHNLIHEDNDMAAVNTYAMEEK 530
DB 477 VMPYESAGLKDVVNLGREGTLLTAHQPWTGAYMMCHNLIHEDNDMAAVNTYAMEEK 536
QY 531 GYLQ-EDFEDPMNPKRAVPIPNRNDFAKAGNFSSESTARVOELADEPNTLDELLED 589
DB 537 GYNETTFDHPEDPRMSARPTAGDLTARSGIFSEESIRAVNELALEOPISLAQVYAS 596

QY 590 L 590
DB 597 L 597

RESULT 8
AAO18211
ID AAO18211 standard; Protein; 627 AA.

XX AC AAO18211;

XX DT 13-SEP-2002 (first entry)
XX DE B spicifera phenol oxidizing enzyme.

XX KW Phenol oxidizing enzyme; fungus; redox reaction; detergent;
XX KM paper industry; pulp industry; textile; food industry.

XX OS Bipolaris spicifera.

XX PN US6399329-B1.

PD 04-JUN-2002.

XX 21-DEC-1999; 99US-0468578.

XX 12-DEC-1998; 98US-0220871.

XX 23-JUN-1999; 99US-0338723.

XX (GENEX) GENENCOR INT INC.

XX Wang H, Bodle EA;

XX WPI, 2002-498835/53.

XX N-PSDB: AAL47583.

XX New polynucleotides encoding phenol oxidizing enzymes, useful for
XX preventing the transfer of dyes in solution from one textile to another
XX during detergent washing -

XX Claim 1; Fig 3; 37pp; English.

The present invention provides the protein and coding sequences of phenol
oxidizing enzymes from Stachybotrys chartarum, Bipolaris spicifera and
Curvularia pallescens. These enzymes are useful in the textiles, paper,
pulp, detergent and food industries. In particular they are useful for
preventing the transfer of dyes in solution from one textile to another
during detergent washing (dye transfer inhibition). The present sequence
is the B. spicifera phenol oxidizing enzyme.

Sequence 627 AA;

Query Match 61.3%; Score 1954.5; DB 23; Length 627;
Best Local Similarity 61.1%; Pred. No. 1e-179;
Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8;

QY 2 LFKSMQLAAAGSLGVLGIPMDGSHPIEAVDEPVKTEVADSLAAAGD----- 53
DB 6 LFSALQLVLS---LAKGITGVAL--SERPAKVDNTPDEKAA--LASTVEDDPADVNM 58
QY 54 -DMESPYNLLRYNALPIPVKOPKMITNPVTKDVIYVEIEIKPFOQRIYPTLRPATL 112
DB 59 KDMQSPERPLIFRQPLPIPAKEPNK-LTNVTKKEIWEYELVIAKPFQGYPSLRPARL 117

QY 113 VGYDGMSPGPTFNPRGTEYVVRFLNNATVENSVHLGSPSRAPFDGMAEDVTPPEGYKD 172
DB 118 VGYGISPGPTIIVPRGTEAVVRFLNODRESSIHLGSPSRAPFDGMAEDVTPPEGYKD 177
QY 173 YYPFNQOSARLLMWDHAFMKTAENAYFGAGATYINDAEDALGSPGYGEFDPIPLLT 232
DB 178 YYPFNQOSARLLMWDHAFMKTAENAYFGAGATYINDAEDALGSPGYGEFDPIPLLT 237

QY 233 AKYNNADGTLRSTEGEDQDLMDVYIHVNGQWPPELVNQPRKRYRFRFLNAAVSRAVLTYLV 292
DB 238 SKYYNADGTLRSTEGEDQDLMDVYIHVNGQWPPELVNQPRKRYRFRFLNAAVSRAVLTYLV 297
QY 293 RTSSPNVRIIPROVIAASDAGLLQAPVQTSNLYLAVEREYIITFTNAGQTLDIRNAET 352
DB 298 KQDNTATRLPPOVIAASDAGLLTHHPVQTSNLYLAVEREYIITFTNAGQTLDIRNAET 357

QY 353 NDVDEDEYARTLEVMRNVVSSGTEVENSQVPTLRDVPFPKKEGPAKDKFKPERSNGH 412
DB 358 NGIGTDDYANTDKVMREHVSQTVVDSVVPBLSQIOPADKT-DIDHFRHRTNGE 416
QY 413 YLINDVGADVNERVLAKPELGTEVEWELNENSSGWSHPVHILHVEFKILRTGSGO-- 470
DB 417 WRINGIGADVNERVLAKPELGTEVEWELNENSSGWSHPVHILHVEFKILRTGSGO-- 476

QY 471 VMPYESAGLKDVVNLGREGTLLTAHQPWTGAYMMCHNLIHEDNDMAAVNTYAMEEK 530
DB 477 VMPYESAGLKDVVNLGREGTLLTAHQPWTGAYMMCHNLIHEDNDMAAVNTYAMEEK 536
QY 531 GYLQ-EDFEDPMNPKRAVPIPNRNDFAKAGNFSSESTARVOELADEPNTLDELLED 589
DB 537 GYNETTFDHPEDPRMSARPTAGDLTARSGIFSEESIRAVNELALEOPISLAQVYAS 596

XX	Claim 8; Fig 10; 45pp; English.
PS	
xx	

This sequence is the Curvularia pallescens phenol oxidizing enzyme. Phenol oxidizing enzymes encoded by nucleic acid sequences which hybridize to the Stachybotrys chartarum DNA (AA51313) are claimed, as long as the enzyme is capable of modifying the colour associated with dyes or coloured compounds. The enzymes are useful in detergent compositions and for modifying colors associated with dyes or coloured compounds which occur in stains in a sample. The enzymes are also useful for pulp and paper bleaching, anti-dye transfer in detergent and other textile applications.

SQ Sequence 627 AA;

Query Match	Score	DB	Length
60.58;	1929.5;	21;	627;

Best Local Similarity 60.5%; Pred. No. 2.6e-177;

Matches 364; Conservative 81; Mismatches 134; Indels 23; Gaps 9;

QY	LFESMQLAAASGLSLSGLVLIIPMDTGSHPLEAVDPVKTEVPADSLTAAAGD-----	53
Db	2 LFESMQLAAASGLSLSGLVLIIPMDTGSHPLEAVDPVKTEVPADSLTAAAGD-----	53
QY	6 LFSALQLAS---IAKGYIVAL--SERPAKTYIDEPPEDEKA--LAAIVEDPDAVVRIL	58
QY	54 -DMESPYYLIRNALRIPRPVKOPKMIITNPYGDWIVYEIKPFQOIRYIPLRPAVL	112
Db	59 KDMOSEPEYILIFREALRIPRAKEPKN-KTNPEKTEIWEYIVAIKPFNOQYPSLRPARL	117
QY	113 VGDGMSPPPTENVPRGETYVRFRLNNMTVENSYLHSSPSRAPFDGAEIVYTPGEXKD	172
Db	118 VGDGIDSPBPTIIVPRGETAAYVRFVNOGDRESHLHSSPSRAPFDGAEOLIMKGQFKD	177
QY	173 YYPEPNQASARLLMYHDHAFMKTAENAYFGQAGAVIINDADALGLSPGYCEPDPIILT	222
Db	178 YYPYNNQARARFLMYHDHAMHTYAENAYFGQAGAVIILTRPADALGLSPGYCKYDIPVLS	237
QY	233 AKTYNADGLRSTEGEDODMGDVITHVNGQWPRFLINVPKRYRFRFLNAAVSRAMLLYLV	292
Db	238 SKRYNSDGLTQTSVEDENSLMGDVITHVNGQWPFENVEPRKRYRLRFLNAAVSRNFAFLYV	297
QY	293 RFSPPVNRIPRFQVIASDAGLLQAPQTSNKLVAAREIILIDTTFNAGOTLDLRNAET	352
Db	298 KQATATRLRPFQVIASDAGLLRHPQTSIDIYAAERLEYLFDAPYAGOTIDLRNKA	357
QY	353 NDVGDEDEXARTLEVMARFVYSSGTEVDNSOVPSLRDPPRPHKEGPADEKFEKRSNGH	412
Db	358 NGVGTEDDDAANDKAYMAREFVSSQAVLVDSVYPAQLSQIQPADKTG-IDHNFRRHNSE	416
QY	413 YLILNMGFADVMERYIARLDELGTVEYVWELMSSGSGMSPHVIHLVDYKILKRTGG---	469
Db	417 WRKNGEFDVQNRILIAKVRPGTYELWELMSSGSGMSPHIVHLVDYFVYARVGDESTRG	476
QY	470 QVMPYESALIKYVWLGRGETLLEIAHNYOPTMGAVYMHCHNLIHEDNDMAAVFYVTAMEE	529
Db	477 -VMPEFSAKLYVWLGRHEIYLYZAHNAPMDGYIMFCHNLIHEDNDMAAIFDYVKLQ	535
QY	530 KGILO-EDFEDPMARPMKRAVYVNRNDFHARAGNFSASTARVOELAEQBYNRLDEILE	588
Db	536 FGYNETTDEHDEDSRMSARPEPTADILARSGIFSEASIRARVWELAEQYPSLQAQVTA	595
QY	589 DL 590	
Db	596 SL 597	

Search completed: July 1, 2003, 10:38:51
Job time : 75 secs

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OM protein - protein search, using sw model

Run on: July 1, 2003, 10:37:36 ; Search time 26 Seconds
(Without alignments)
672.201 Million cell updates/sec

Title: US-10-080-233-2

Perfect score: 3189
Sequence: 1 MLEFSWQLAASGLSGVLG.....AEQPYNRDLDELIDGIEE 594

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Number of hits satisfying chosen parameters: 262574

262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents AA:
1: /cgml2_6/prodata/1/aa/5A.COMB.pep.*
2: /cgml2_6/prodata/1/aa/5B.COMB.pep.*
3: /cgml2_6/prodata/1/aa/6A.COMB.pep.*
4: /cgml2_6/prodata/1/aa/6B.COMB.pep.*
5: /cgml2_6/prodata/1/aa/PCITUS.COMB.pep.*
6: /cgml2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3189	100.0	594	US-09-468-578-2	Sequence 2, Appl1
2	3189	100.0	594	US-09-218-702-2	Sequence 2, Appl1
3	1954.5	61.3	627	US-09-468-578-4	Sequence 4, Appl1
4	1929.5	54.1	627	US-09-468-578-7	Sequence 7, Appl1
5	1724.5	54.1	572	US-09-401-476-2	Sequence 4, Appl1
6	1716.5	53.7	583	US-09-401-476-2	Sequence 2, Appl1
7	1712.5	53.8	568	US-09-218-702-4	Sequence 4, Appl1
8	400.5	12.6	322	US-09-134-001C-2946	Sequence 2946, Ap
9	357.5	11.2	114	US-09-468-578-9	Sequence 9, Appl1
10	202	6.3	616	US-08-749-882A-2	Sequence 2, Appl1
11	202	6.3	616	US-08-539-134-2	Sequence 2, Appl1
12	202	6.3	616	US-08-991-531-2	Sequence 2, Appl1
13	202	6.3	616	US-09-032-315-9	Sequence 9, Appl1
14	202	6.3	616	US-08-993-318A-9	Sequence 9, Appl1
15	202	6.3	616	US-09-028-887-2	Sequence 2, Appl1
16	202	6.3	616	US-09-399-886-9	Sequence 9, Appl1
17	202	6.3	616	US-09-396-260-9	Sequence 9, Appl1
18	202	6.3	616	US-09-518-901-2	Sequence 2, Appl1
19	202	6.3	616	US-09-576-281-9	Sequence 9, Appl1
20	198.5	6.2	529	US-08-172-331B-14	Sequence 14, Appl1
21	198.5	6.2	529	US-08-706-037-25	Sequence 25, Appl1
22	198.5	6.2	529	US-09-005-397-25	Sequence 25, Appl1
23	198.5	6.2	529	US-09-032-315-5	Sequence 5, Appl1
24	198.5	6.2	529	US-08-993-318A-5	Sequence 5, Appl1
25	198.5	6.2	529	US-09-399-886-5	Sequence 5, Appl1
26	198.5	6.2	529	US-09-386-260-5	Sequence 5, Appl1
27	198.5	6.2	529	US-09-576-281-5	Sequence 5, Appl1

28	198	6.2	620	1	US-08-940-661A-2	Sequence 2, Appl1
29	198	6.2	620	2	US-09-083-485-2	Sequence 2, Appl1
30	198	6.2	620	2	US-08-939-218A-2	Sequence 2, Appl1
31	197	6.2	573	2	US-08-991-531-1	Sequence 1, Appl1
32	197	6.2	573	2	US-09-032-315-10	Sequence 10, Appl1
33	197	6.2	573	2	US-08-993-318A-10	Sequence 10, Appl1
34	197	6.2	573	3	US-09-028-887-1	Sequence 1, Appl1
35	197	6.2	573	4	US-09-399-886-10	Sequence 10, Appl1
36	197	6.2	573	4	US-09-396-260-10	Sequence 10, Appl1
37	197	6.2	573	4	US-09-518-901-1	Sequence 1, Appl1
38	197	6.2	573	4	US-09-576-281-10	Sequence 10, Appl1
39	197	6.2	616	5	PCT-US95-06816-2	Sequence 2, Appl1
40	197	6.2	620	1	US-08-706-037-27	Sequence 27, Appl1
41	197	6.2	620	2	US-09-005-397-27	Sequence 27, Appl1
42	197	6.2	620	5	PCT-US95-06815-2	Sequence 2, Appl1
43	194	6.1	511	1	US-08-462-484-8	Sequence 8, Appl1
44	194	6.1	511	1	US-08-441-147-8	Sequence 8, Appl1
45	194	6.1	511	5	PCT-US95-07536-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1						
US-09-468-578-2						
Sequence 2, Application US/09468578						
Patent No. 6399329						
GENERAL INFORMATION:						
APPLICANT: Wang, Huang						
TITLE OF INVENTION: Phenol Oxidizing Enzymes						
FILE REFERENCE: GC561-3						
CURRENT APPLICATION NUMBER: US/09/468,578						
PRIOR FILING DATE: 1999-12-21						
PRIOR APPLICATION NUMBER: US 09/220,871						
PRIOR FILING DATE: 1998-12-23						
PRIOR APPLICATION NUMBER: US 09/338,723						
PRIOR FILING DATE: 1999-06-23						
NUMBER OF SEQ ID NOS: 17						
SOFTWARE: FastSeq for Windows Version 4.0						
SEQ ID NO 2						
LENGTH: 594						
TYPE: PRT						
ORGANISM: Stachybotrys chartarum						
US-09-468-578-2						
Query Match						
Best local Similarity 100.0%; Score 3189; DB 4; Length 594;						
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	MLEFSWQLAASGLSGVLGIPMDTGSHPITAVPEVKTETVFADSLAAAGDDDMWESP	60			
DB	1	MLEFSWQLAASGLSGVLGIPMDTGSHPITAVPEVKTETVFADSLAAAGDDDMWESP	60			
QY	61	NLRYRNLPIPVKQPMIITNPTGDIWYEIEIRPFQRIPTLRPATLVGDMSP	120			
DB	61	NLRYRNLPIPVKQPMIITNPTGDIWYEIEIRPFQRIPTLRPATLVGDMSP	120			
QY	121	GPTFNVRGTEVTVRFINNATVENSYHLHSPSPAPDGAEDVTFPEKTKDYFPNQS	180			
DB	121	GPTFNVRGTEVTVRFINNATVENSYHLHSPSPAPDGAEDVTFPEKTKDYFPNQS	180			
QY	181	ARLWYHDHAFMKRAENAYGQACAYIINDAEALGLPSGGEFDIPLITATKYNDG	240			
DB	181	ARLWYHDHAFMKRAENAYGQACAYIINDAEALGLPSGGEFDIPLITATKYNDG	240			
QY	241	TLRSTEGEDDLMGDVIVHNGQPPFLNVQPRKXRFRLNAAVSRAMLLYLVRTSSPNR	300			
DB	241	TLRSTEGEDDLMGDVIVHNGQPPFLNVQPRKXRFRLNAAVSRAMLLYLVRTSSPNR	300			
QY	301	IPFOVIASDAGLLOAPVQTSNLYLAVEREIIITDFNFAQGITDLRNVAETNDVGDE	360			
DB	301	IPFOVIASDAGLLOAPVQTSNLYLAVEREIIITDFNFAQGITDLRNVAETNDVGDE	360			

Query Match 100.0%; Score 3189; DB 4; Length 594;
Best Local Similarity 100.0%; Pred. No. 1.5e-308;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MLFWSQMLAAAGSLGVLGIPMDGSHPIEAVDEPVKTEVPADSLAAAGDDMESPPY 60
Db 1 MLFWSQMLAAAGSLGVLGIPMDGSHPIEAVDEPVKTEVPADSLAAAGDDMESPPY 60

Query 61 NLTYNNALPIPPVKOPKMITNPVTGKDIWYEIEIKRFOQRITPILRPATLVGYDQMS 120
Db 61 NLTYNNALPIPPVKOPKMITNPVTGKDIWYEIEIKRFOQRITPILRPATLVGYDQMS 120

Query 61 NLTYNNALPIPPVKOPKMITNPVTGKDIWYEIEIKRFOQRITPILRPATLVGYDQMS 120
Db 61 NLTYNNALPIPPVKOPKMITNPVTGKDIWYEIEIKRFOQRITPILRPATLVGYDQMS 120

Query 121 GPTFNVPRGTEVTVRFINNATVENSVLHGSFSPRAPFDGMAEDVTFPGSEYKDYFPNTQS 180
Db 121 GPTFNVPRGTEVTVRFINNATVENSVLHGSFSPRAPFDGMAEDVTFPGSEYKDYFPNTQS 180

Query 121 GPTFNVPRGTEVTVRFINNATVENSVLHGSFSPRAPFDGMAEDVTFPGSEYKDYFPNTQS 180
Db 121 GPTFNVPRGTEVTVRFINNATVENSVLHGSFSPRAPFDGMAEDVTFPGSEYKDYFPNTQS 180

Query 181 ARLLYHHAHMKTKTENAAYFGQAGAYIINDEADALGIPSGYGEEDIPILTLAKYNNADG 240
Db 181 ARLLYHHAHMKTKTENAAYFGQAGAYIINDEADALGIPSGYGEEDIPILTLAKYNNADG 240

Query 241 TLRTSGEGDODLMDGVHIVNGQPPFLVNOQPKRYRFRFLNAVSRAMLLYLRTSSPNVR 300
Db 241 TLRTSGEGDODLMDGVHIVNGQPPFLVNOQPKRYRFRFLNAVSRAMLLYLRTSSPNVR 300

Query 241 TLRTSGEGDODLMDGVHIVNGQPPFLVNOQPKRYRFRFLNAVSRAMLLYLRTSSPNVR 300
Db 241 TLRTSGEGDODLMDGVHIVNGQPPFLVNOQPKRYRFRFLNAVSRAMLLYLRTSSPNVR 300

Query 301 IPFOVIASDAGILQAPVOTSNLYLAVEREYIITDFTNAGOTLDRNVAETNDVDEDE 360
Db 301 IPFOVIASDAGILQAPVOTSNLYLAVEREYIITDFTNAGOTLDRNVAETNDVDEDE 360

Query 301 IPFOVIASDAGILQAPVOTSNLYLAVEREYIITDFTNAGOTLDRNVAETNDVDEDE 360
Db 301 IPFOVIASDAGILQAPVOTSNLYLAVEREYIITDFTNAGOTLDRNVAETNDVDEDE 360

Query 361 YARLEVMRFVYSSSTVEDNSQVSTLNDVPPRPKREGPADKHFFERSNGHYLLINDVGF 420
Db 361 YARLEVMRFVYSSSTVEDNSQVSTLNDVPPRPKREGPADKHFFERSNGHYLLINDVGF 420

Query 421 ADVNERVLAKPELGIVEVWELENSGSGMHPVHILVDFKILKRTGRCQVVPYESAGLK 480
Db 421 ADVNERVLAKPELGIVEVWELENSGSGMHPVHILVDFKILKRTGRCQVVPYESAGLK 480

Query 421 ADVNERVLAKPELGIVEVWELENSGSGMHPVHILVDFKILKRTGRCQVVPYESAGLK 480
Db 421 ADVNERVLAKPELGIVEVWELENSGSGMHPVHILVDFKILKRTGRCQVVPYESAGLK 480

Query 481 DVVWLGREGETILIEAHYOPTGAYMCHNLIHEDNDMAAVFNVTAMEEKGYLQEDFEDP 540
Db 481 DVVWLGREGETILIEAHYOPTGAYMCHNLIHEDNDMAAVFNVTAMEEKGYLQEDFEDP 540

Query 541 MNPKRAVPYNNRNDPHARAGNFSASITARVOELAEQEPYNNRLDEILDGIEE 594
Db 541 MNPKRAVPYNNRNDPHARAGNFSASITARVOELAEQEPYNNRLDEILDGIEE 594

Query 541 MNPKRAVPYNNRNDPHARAGNFSASITARVOELAEQEPYNNRLDEILDGIEE 594
Db 541 MNPKRAVPYNNRNDPHARAGNFSASITARVOELAEQEPYNNRLDEILDGIEE 594

Query Match 61.3%; Score 1954.5; DB 4; Length 627;
Best Local Similarity 61.1%; Pred. No. 1.3e-185;
Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8;

Query 2 LFKSQMLAAAGSLGVLGIPMDGSHPIEAVDEPVKTEVPADSLAAAGDDMESPPY 53
Db 2 LFKSQMLAAAGSLGVLGIPMDGSHPIEAVDEPVKTEVPADSLAAAGDDMESPPY 53

Query 54 -DWESPPNLYNNALPIPPVKOPKMITNPVTGKDIWYEIEIKRFOQRITPILRPATLV 112
Db 54 -DWESPPNLYNNALPIPPVKOPKMITNPVTGKDIWYEIEIKRFOQRITPILRPATLV 112

Query 59 KDMQSPFELPIRQPLPIPPAKPEPK-LTNPTNKEIYELVIRFTQOQVPSLRPARL 117
Db 59 KDMQSPFELPIRQPLPIPPAKPEPK-LTNPTNKEIYELVIRFTQOQVPSLRPARL 117

Query 113 VGYDMSGPTFNVPRGTEVTVRFINNATVENSVLHGSFSPRAPFDGMAEDVTFPGSEYK 172
Db 113 VGYDMSGPTFNVPRGTEVTVRFINNATVENSVLHGSFSPRAPFDGMAEDVTFPGSEYK 172

Query 118 VGYDMSGPTFNVPRGTEVTVRFINNATVENSVLHGSFSPRAPFDGMAEDVTFPGSEYK 172
Db 118 VGYDMSGPTFNVPRGTEVTVRFINNATVENSVLHGSFSPRAPFDGMAEDVTFPGSEYK 172

Query 173 YTFPNYQASRLIWHYHDAHFMKTAEATYFGQAGAYIINDEADALGIPSGYGEEDIPIL 232
Db 173 YTFPNYQASRLIWHYHDAHFMKTAEATYFGQAGAYIINDEADALGIPSGYGEEDIPIL 232

Query 178 YTFPNYQASRLIWHYHDAHFMKTAEATYFGQAGAYIINDEADALGIPSGYGEEDIPIL 232
Db 178 YTFPNYQASRLIWHYHDAHFMKTAEATYFGQAGAYIINDEADALGIPSGYGEEDIPIL 232

Query 233 AKYNAAGTTLSTEGEDODLMDGVHIVNGQPPFLVNOQPKRYRFRFLNAVSRAMLLYL 292
Db 233 AKYNAAGTTLSTEGEDODLMDGVHIVNGQPPFLVNOQPKRYRFRFLNAVSRAMLLYL 292

Query 238 SKTYNADGTLKTSVGEDKSWMGDILHVGQPPFLVNOQPKRYRFRFLNAVSRAMLLYL 297
Db 238 SKTYNADGTLKTSVGEDKSWMGDILHVGQPPFLVNOQPKRYRFRFLNAVSRAMLLYL 297

Query 293 RTSSPNVRIIPFOVIASDAGILQAPVOTSNLYLAVEREYIITDFTNAGOTLDRNVAET 352
Db 293 RTSSPNVRIIPFOVIASDAGILQAPVOTSNLYLAVEREYIITDFTNAGOTLDRNVAET 352

Query 298 KODNATATLPRQVIAASDAGILHLPVQTSDMYAAVEREYIYFDFAPYAGOTLDRNFAKA 357
Db 298 KODNATATLPRQVIAASDAGILHLPVQTSDMYAAVEREYIYFDFAPYAGOTLDRNFAKA 357

Query 333 NDVGEDEYARTLEVMRFVYSSSTVEDNSQVSTLNDVPPRPKREGPADKHFFERSNGH 412
Db 333 NDVGEDEYARTLEVMRFVYSSSTVEDNSQVSTLNDVPPRPKREGPADKHFFERSNGH 412

Query 338 NGITGDDDYANTMDKMYRHHVSQTFVDDNSVYPEOLSOQFPAKDT-DIDHFRFRHRTGE 416
Db 338 NGITGDDDYANTMDKMYRHHVSQTFVDDNSVYPEOLSOQFPAKDT-DIDHFRFRHRTGE 416

Query 413 YLINDVGRADVNERVLAKPELGIVEVWELENSGSGMHPVHILVDFKILKRTGRCQV 470
Db 413 YLINDVGRADVNERVLAKPELGIVEVWELENSGSGMHPVHILVDFKILKRTGRCQV 470

Query 417 WRINIGFADVNERVLAKPELGIVEVWELENSGSGMHPVHILVDFKILKRTGRCQV 476
Db 417 WRINIGFADVNERVLAKPELGIVEVWELENSGSGMHPVHILVDFKILKRTGRCQV 476

Query 471 VMPYESAGLKDVVWLGREGETILIEAHYOPTGAYMCHNLIHEDNDMAAVFNVTAMEEK 530
Db 471 VMPYESAGLKDVVWLGREGETILIEAHYOPTGAYMCHNLIHEDNDMAAVFNVTAMEEK 530

Query 477 VMPYESAGLKDVVWLGREGETILIEAHYOPTGAYMCHNLIHEDNDMAAVFNVTAMEEK 536
Db 477 VMPYESAGLKDVVWLGREGETILIEAHYOPTGAYMCHNLIHEDNDMAAVFNVTAMEEK 536

Query 531 GYLQ-EDFEDPNNPKRAVPYNNRNDPHARAGNFSASITARVOELAEQEPYNNRLDEILD 589
Db 531 GYLQ-EDFEDPNNPKRAVPYNNRNDPHARAGNFSASITARVOELAEQEPYNNRLDEILD 589

Db 537 GYNETTFHDPEDPMSARPTAGDILARSIFSEESIRARVNEALAEQPSYSLAQYAS 596
 Oy 590 L 590
 Db 597 L 597

RESULT 4
 US-09-468-578-7
 ; Sequence 7, Application US/09468578
 ; Patent No. 6399329
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Huaming
 ; APPLICANT: Bodle, Elizabeth A.
 ; TITLE OF INVENTION: Phenol Oxidizing Enzymes
 ; FILE REFERENCE: GC561-3
 ; CURRENT APPLICATION NUMBER: US/09/468,578
 ; CURRENT FILING DATE: 1999-12-21
 ; PRIOR APPLICATION NUMBER: US 09/220,871
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: US 09/338,723
 ; PRIOR FILING DATE: 1999-06-23
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 627
 ; TYPE: PRF
 ; ORGANISM: Curvularia pallescens.
 US-09-468-578-7

Query Match 60.5%; Score 1929.5; DB 4; Length 627;
 Best Local Similarity 60.5%; Pred. No. 3,9e-183;
 Matches 364; Conservative 81; Mismatches 134; Indels 23; Gaps 9;

Oy 2 LFSKQDLAASGLSGYLGPMDTGHPIEAVDPEKTEVFADSLAAGD----- 53
 Db 6 LFSALDAS---IAKGIYVAL--SERPAKYIDETDEEKAA--LAAIVDDPADYPRIL 58
 Oy 54 -DSEPPYNLRYNAPLPVPKPKMTITNPYTKDIXWYEIEIKPKQOIRPYLPRLATL 112
 Db 59 KQMSPEYPLFREALPIPAKEPK-MTPVTKELWYEIYIKPNQOYVSLRPARL 117
 Oy 113 VGYDMSPGPTFNVPRGTETVRFINNATVENSVHLGSPSRAPFDMAEDVTPPEGYK 172
 Db 118 VGDGISPGPTIIVPRGTEAVRFVNGDRESSIHLGSPSRAPFDMAEDLWKQGFKD 177
 Oy 173 YYPNPQASRLWYHHAFAKTAENAYFGAGAYIINDEADALGSPGGEPIRLT 232
 Db 178 YYPNNQAAFLWYHHAFAKTAENAYFGAGAYIITDPAEDALGSPGKYDIPYLS 237
 Oy 233 AKYNNADGTLRSTEGEDODLMDGVYIHVNGQPMFPLANVQPRKYPREFLNAVSRAMLTYLV 292
 Db 238 SKRYNSDGTQTSVGEDNSLMDGVYIHVNGQPMFPEFNVPRKYLRLFLNAAVSRFALYFV 297
 Oy 293 RISSPVNRIPEOVIASDAGLLQAPVOTSNLYLAVERXEIITIDFTNAGOTLDRVAET 352
 Db 298 KQATATRLRPFQVIASDAGLLTHPVQTSIDYVAAREYEIVDFAPAPAGOTIDLRNPAKA 357
 Oy 353 NDVGDEDEYARTLEVAFVYSSGTVEDNSQVPSLRLVPRPPRKEGADKHEKFRSNGH 412
 Db 358 NGVGTDDDYANTKRFHVSQAAYVDSVYPAQLSQIOPADKTG-IDHFRHRRTNSE 416
 Oy 413 YLLNDVGFADVNERVLAKEPLGTVVEWLENSGGWSHPVHILHYDKIILKRGSG--RG 469
 Db 417 WRINGIGFADVQRIILAKVPRGTVELEWLENSGGWSHPVHILHYDRVVAARYGDESTRG 476
 Oy 470 QVAPYESAGLKVYVLMGSETLTLEAHYQPTGAYMMHCHNLIHEDNDMAVFNVTAMEE 529
 Db 477 -VAPYESAGLKVYVLMGSETLTLEAHYQPTGAYMMHCHNLIHEDNDMAVFNVTAMEE 535
 Oy 530 KGYLQ-EDFEDPMKRAVPYKRNDFHARAGNFSASITARVOELAEQPYNRIDILE 588
 Db 536 FGNETTDFHDPEDSRMSARPTAGDILARSIFSEESIRARVNEALAEQPSYSLAQYAS 595

Oy 589 DL 590
 Db 596 SL 597

RESULT 5
 US-09-401-476-4
 ; Sequence 4, Application US/09401476
 ; Patent No. 6168936
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Huaming
 ; APPLICANT: Bodle, Elizabeth A.
 ; TITLE OF INVENTION: Phenol Oxidizing Enzymes
 ; FILE REFERENCE: GC584
 ; CURRENT APPLICATION NUMBER: US/09/401,476
 ; CURRENT FILING DATE: 1999-09-22
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 572
 ; TYPE: PRF
 ; ORGANISM: Stachyotrys charatum
 US-09-401-476-4

Query Match 54.1%; Score 1724.5; DB 4; Length 572;
 Best Local Similarity 60.3%; Pred. No. 8.6e-163;
 Matches 322; Conservative 75; Mismatches 128; Indels 9; Gaps 7;

Oy 57 SPYNYLLRYNAPLPVPKPKMTITNPYTKDIXWYEIEIKPKQOIRPYLPRLATLVGYD 116
 Db 43 SPQYP-MFTVPLPIPVKOPRLVTNPNVNGOEWYEVWEIYKPYHQYVPLGSDLVGYD 101
 Oy 117 GMSPGPTFNVPRGTETVRFINNATVENSVHLGSPSRAPFDMAEDVTPPEGYKDYYP 176
 Db 102 GMSPGPTFNVPRGTETVRFINNATVENSVHLGSPSRAPFDMAEDVTPPEGYKDYYP 161
 Oy 177 NYQASRLWYHHAFAKTAENAYFGAGAYIINDEADALGSPGGEPIRLTATKY 236
 Db 162 NRGASRLWYHHAFAKTAENAYFGAGAYIINDEADALGSPGGEPIRLTATKY 221
 Oy 237 NADGTLRSTEGEDODLMDGVYIHVNGQPMFPLANVQPRKYPREFLNAVSRAMLTYVTS 296
 Db 222 TANGLNLTYNGLNLSFNGDVIHNGQPMFPEFNVPRKYLRLFLNAAVSRFALYFV 281
 Oy 297 PNVPYIPROYASDAGLLQAPVOTSNLYLAVERXEIITIDFTNAGOTLDRVAET 355
 Db 282 IDTRLPRKVIASDGLLEHRAOTSLIISNAEREYVFDPSDYAGKTIELRNIGSGTIGI 341
 Oy 356 GDEDEYARTLEVAFVYSSGTVEDNSQVPSLRLVPRPPRKEGADKHEKFRSNGHY 413
 Db 342 GTDIDYDNTDKVMRFVVAADTQDTSVVPANLUDVFPSPSTNTPT--RQPRFGRTGPTW 399
 Oy 414 LINDVGFADVNERVLAKEPLGTVVEWLENSGGWSHPVHILHYDKIILKRGSG--QY 471
 Db 400 TINGVAFADVQNRILANVPVGTVERWELINAGNMTIHLHLDVFIYSTSGNNARTV 459
 Oy 472 MPYASAGLKVYVLMGSETLTLEAHYQPTGAYMMHCHNLIHEDNDMAVFNVTAMEEK 531
 Db 460 MPYAS-GLKDVYVLMGSETLTLEAHYQPTGAYMMHCHNLIHEDNDMAVFNVTAMEEK 518
 Oy 532 YLQDFEDPMKRAVPYKRNDFHARAGNFSASITARVOELAEQPYNRIDILE 585
 Db 519 YNATVFPDPMELMQARPELGEQAGSGQSVQAVTERIOTYMAEYRYAAADE 572

RESULT 6
 US-09-401-476-2
 ; Sequence 2, Application US/09401476
 ; Patent No. 6168936
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Huaming
 ; APPLICANT: Bodle, Elizabeth A.
 ; TITLE OF INVENTION: Phenol Oxidizing Enzymes
 ; FILE REFERENCE: GC584

Db 64 IODKTE-VSKLNYSTKDEDTGDTVLVNGIVNPKLTAKEERIKRLRLNGSNARDLNT 122
 QY 290 YLVRTSSPNVRIPROYIASDAGLLQAPVQTSNLYVAERETIIPFTNAGOTLDLRYN 349
 Db 123 KLSNNOS-----FETIASDGLKNAKKLKEINLAPSEKKEIVIDLSKKGEKISL--- 173
 QY 350 AETNDVDEDEDEARTELVNMFVSSGTVEDNSQVPTLRDPPRPHKEGPADEHFKERS 409
 Db 174 -----VDNDK-----TVLLPISNKEKSSNKGNTPK-----VSKKIKLEGM 208
 QY 410 NGHYLINDVGFADVNERVLAKPELGVEWELEN---SSGWSHPVHILVDKRIKRTG 466
 Db 209 NDHVTINGNKF-DPN-RIDFTQKLNQKEVWEIENVKDKMGKMKHPEHIGTOFKVLSVD- 265
 QY 467 GRCQVMPYESAGKDVWVLRGETLITLTAHYQPTWAGYMHCHNLHEDDMAVFTV 525
 Db 266 --GEKPKDMRGKAKDVISLEPGQKAKIEVEFKN-TGYMHCHILHEHEDGMGQIKVT 321

ULT 9
 09-468-578-9
 Sequence 9, Application US/09468578
 Patent No. 6393329

GENERAL INFORMATION:
 APPLICANT: Wang, Huang
 APPLICANT: Bodie, Elizabeth A.
 TITLE OF INVENTION: Phenol Oxidizing Enzymes
 FILE REFERENCE: GC561-3
 CURRENT APPLICATION NUMBER: US/09/468,578
 PRIOR FILING DATE: 1999-12-21
 PRIOR APPLICATION NUMBER: US 09/220,871
 PRIOR FILING DATE: 1998-12-23
 PRIOR APPLICATION NUMBER: US 09/338,723
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 9
 LENGTH: 114
 TYPE: PRF
 ORGANISM: Amersporium atrum
 NAME/KEY: VARIANT
 LOCATION: (1)...(114)
 OTHER INFORMATION: Xaa = space of unknown number of aa
 US-09-468-578-9

Query Match 11.2%; Score 357.5; DB 4; Length 114;
 Best Local Similarity 32.2%; Pred. No. 6.8e-28;
 Matches 85; Conservative 13; Mismatches 15; Indels 151; Gaps 4;
 Db 194 TBNATFGGAGAYIINDEADALGSPGGEPIPLITAKYYNADGTLSTEGEQDLM 253
 1 TBNATFGGAGAYIINDEADALGSPGGEPIPLITAKYYNADGTLSTEGEQDLM 253
 Db 254 GDVIVHNGQWPELNVQPKRYRFLNAAVSRAMLLYLVTSPPNVRIPROYIASDAGL 313
 59 GDVIVHNGQWPELNVQPKRYRFLNAAVSRAMLLYLVTSPPNVRIPROYIASDAGL 313
 QY 314 QAPVQTSNLYVAERETIIPFTNAGOTLDLRYNVAETNDVDEDEARTELVNMFVSS 373
 Db 92 ----- 91
 QY 374 SGTVEDNSQVPTLRDPPRPHKEGPADEHFKERSNGHYLINDVGFADVNERVLAKPEL 433
 Db 92 -----FK----- 93
 QY 434 GVEWELEN-SSGWSHPVHIL 456
 Db 94 ---XVMELEWTSNGWSYVPHIL 114

RESULT 10
 US-08-749-882A-2

Sequence 2, Application US/08749882A
 Patent No. 5750388
 GENERAL INFORMATION:
 APPLICANT: Betka, Randy
 APPLICANT: Thompson, Sheryl
 APPLICANT: Xu, Feng
 TITLE OF INVENTION: Purified Scytalidium Laccases
 TITLE OF INVENTION: And Nucleic Acids Encoding Same
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 5750388 No. 5750388disk Of No. 5750388th America, Inc.
 STREET: 405 Lexington Avenue - 64th Fl.
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10174
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/749,882A
 FILING DATE: 15-NOV-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Lambiris, Elias J
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 4186.020-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-878-9652
 TELEFAX: 212-878-9655
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 616 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Scytalidium thermophilum
 US-08-749-882A-2

Query Match 6.3%; Score 202; DB 1; Length 616;
 Best Local Similarity 23.1%; Pred. No. 3.4e-11;
 Matches 147; Conservative 77; Mismatches 237; Indels 174; Gaps 35;
 Db 8 LAAASGLT-SGVLTGIPMDTGSHPLEAVDPVKEVFADSLAAAGDDWSPPYNLYRN 66
 9 LLLAGLNSGALAAP---STHP--RSNPDLLEBDHSLTSRQG--SCHSPNRACWCS 61
 QY 67 ALPIPPKQKMTITNVTGKDIWYETIEIKPQOQRIY--TLRPATLVIGDMSQPTF 124
 62 GFIDINDYETK---TPNTGV-VRRYTFDTEVDNRPQGVVKEKMLINDKL-LGTV 115
 Db 125 NVDRGTETVVRFINN--ATVENSVHLHGSRPAP--FDGWAEDVTF-----PGEYKDYFP 176
 116 FANWG-DTIEVYVNNHILRTGTSIHMHGLHOKGTNHYDG-ANGVTECPRIIPGSSRYVSFR 173
 Db 177 NYQSAFLWYHDAFMKTAENAFEGGAGAYIINDEADALGSPGGEPIPL-ITLAK- 234
 174 ARQYG-TSMYHSH-FSAQYGN--GVSGALQINGPA---SLP-----YDIDGVLPLD 219
 QY 235 --YTNADGTLRSTEGEQDLMGVIVHNGQ-----FWPLNVP--RKYPFRFLNAA 282
 220 WYKSAQDLVLETLAGNAPFSDNYLINTGAKHPTGEGEYATVKLPDRHRRLRLNMS 279
 Db 283 VSRAMLLYLVRTSSPNVRIPROYIASDAGLLQAPVQTSNLYVAERETIIPFT----- 337
 280 VENHFOVSLAKHT-----MYIADNVYVNA-MYVDSLFMAVGQKTYDTTIDASAQVGN 331
 QY 338 ---NFAQ-----TLDLRYNVAETN 353

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Db      332 YWENTFGGQKCGFSHPAPAAIFRYEGAPDALPTDGAAPKHQCIPTIDLSPVYOKN 391
QY      354 DVGDEDEYARLEVARFVWSSGTVEDNSQVSTLRDVPFPKKEGPADKHFKERSNG-- 411
Db      392 -----VPVDFYKEPG-----NTLPVTL-----HVDQAAPHVFTWKINGS 428
QY      412 -----HYLINDVGFADVNERVLAKPELGTVWELENSSG--NSHPVHILV' 457
Db      429 ADVDMRPRVLEEVNNDLSIPVKNNIIVRVDGVNEMTYWLVENDEGRSLPMPHLMGH 488
QY      458 DEKILKRTGGRCQVMPYESAGL-----KDYVWL-GKGETLTIEAHYQ 498
Db      489 DFEVLGRS--PDVSPDSETRFVDPAYDLPRLRGHNVPYRROVTMLPARGMILLAFRTDN 545
QY      499 PWTGAYMMHCHNLIHEDNDMAVFNVTAMEEKGYL 533
Db      546 P--GAWLFRCHTAMHVSGLSVDFLERPDELRGQL 578

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Run on: July 1, 2003, 10:41:07 ; Search time 51 Seconds
(without alignments)

1277.063 Million cell updates/sec

Title: US-10-080-233-2

Perfect score: 3189

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
9: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
11: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3189	100.0	594	US-09-338-723A-2	Sequence 2, Appl1
2	3189	100.0	594	US-10-080-210-2	Sequence 2, Appl1
3	3189	100.0	594	US-10-080-233-2	Sequence 2, Appl1
4	1854.5	61.3	627	US-09-338-723A-4	Sequence 4, Appl1
5	1854.5	61.3	627	US-10-080-210-4	Sequence 4, Appl1
6	1924.5	60.5	627	US-10-080-210-7	Sequence 7, Appl1
7	1724.5	54.1	572	US-09-942-185-4	Sequence 4, Appl1
8	1716.5	53.8	583	US-09-942-185-2	Sequence 2, Appl1
9	1716.5	53.8	583	US-09-954-385-1	Sequence 1, Appl1
10	1712.5	53.7	568	US-10-080-233-4	Sequence 4, Appl1
11	300	15.7	511	US-09-738-626-4553	Sequence 453, Ap
12	357.5	11.2	114	US-10-080-210-9	Sequence 9, Appl1
13	202	6.3	616	US-09-869-877-9	Sequence 9, Appl1
14	202	6.3	616	US-09-732-350-9	Sequence 9, Appl1
15	198.5	6.2	529	US-09-869-877-5	Sequence 5, Appl1
16	198.5	6.2	529	US-09-732-350-5	Sequence 5, Appl1
17	197	6.2	573	US-09-869-877-10	Sequence 10, Appl1
18	197	6.2	573	US-09-732-350-10	Sequence 10, Appl1
19	192.5	6.0	499	US-09-869-877-2	Sequence 2, Appl1

20	192.5	6.0	499	10	US-09-732-350-2	Sequence 2, Appl1
21	188.5	5.9	520	9	US-10-263-819-2	Sequence 2, Appl1
22	187.5	5.9	539	9	US-09-869-877-1	Sequence 1, Appl1
23	187.5	5.9	539	10	US-09-732-350-1	Sequence 1, Appl1
24	179	5.6	548	10	US-09-869-877-4	Sequence 4, Appl1
25	179	5.6	548	10	US-09-732-350-4	Sequence 4, Appl1
26	174.5	5.5	499	9	US-09-869-877-3	Sequence 3, Appl1
27	174.5	5.5	499	10	US-09-732-350-3	Sequence 3, Appl1
28	171.5	5.4	499	9	US-10-164-775-5	Sequence 5, Appl1
29	162	5.1	564	9	US-09-944-160-12	Sequence 12, Appl1
30	147	4.6	493	9	US-09-738-626-6780	Sequence 6780, Ap
31	126.5	4.0	572	10	US-09-869-877-7	Sequence 7, Appl1
32	126.5	4.0	572	10	US-09-732-350-7	Sequence 7, Appl1
33	121.5	3.8	866	9	US-10-002-3098-2	Sequence 2, Appl1
34	119.5	3.7	575	9	US-09-869-877-8	Sequence 8, Appl1
35	119.5	3.7	575	10	US-09-732-350-8	Sequence 8, Appl1
36	111	3.5	599	10	US-09-869-877-6	Sequence 6, Appl1
37	111	3.5	599	10	US-09-732-350-6	Sequence 6, Appl1
38	105	3.3	2764	9	US-09-808-602-80	Sequence 80, Appl1
39	105	3.3	2764	9	US-09-800-198-68	Sequence 68, Appl1
40	104.5	3.3	1938	9	US-10-014-436-2	Sequence 2, Appl1
41	103.5	3.2	596	9	US-10-213-990-51	Sequence 51, Appl1
42	103	3.2	19	10	US-09-338-723A-6	Sequence 6, Appl1
43	100.5	3.2	19	12	US-10-080-210-10	Sequence 10, Appl1
44	100.5	3.2	1600	9	US-09-738-626-4310	Sequence 4310, Ap
45	100.5	3.2	1653	10	US-09-741-669-402	Sequence 402, App

ALIGNMENTS

RESULT 1
US-09-338-723A-2
Sequence 2, Application US/09338723A
Patent No. US2002019038A1
GENERAL INFORMATION:
APPLICANT: Humming, Wang
TITLE OF INVENTION: Phenol Oxidizing Enzymes
FILE REFERENCE: GC561-2
CURRENT APPLICATION NUMBER: US/09/338,723A
CURRENT FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 09/220,871
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 594
TYPE: PRT
ORGANISM: Stachybotrys chartarum
US-09-338-723A-2

Query Match	100.0%	Score 3189	DB 10	Length 594
Best Local Similarity	100.0%	Pred. No. 2.6e-251		
Matches 594	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MFKSWQLAASGLSGVLGIPMDTGSHPLEAVDEYKTEVFADSLAAGDDWESPYPY 60		
DB	1	MFKSWQLAASGLSGVLGIPMDTGSHPLEAVDEYKTEVFADSLAAGDDWESPYPY 60		
QY	61	NLRYRNALPIPPVQPMIITNPYTGDIWYEIEIRPFOQRIYPTLRPATLVGDMS 120		
DB	61	NLRYRNALPIPPVQPMIITNPYTGDIWYEIEIRPFOQRIYPTLRPATLVGDMS 120		
QY	121	GPFFNVDRGTEVYVRFINNAVENSVLHSPSPAPDGAEDVTFPEGEKDYFPYQS 180		
DB	121	GPFFNVDRGTEVYVRFINNAVENSVLHSPSPAPDGAEDVTFPEGEKDYFPYQS 180		
QY	181	ARLWYVDAFMKTAENYAGCAVYIINDEADALGPGYGEFDIPLITAKYVADG 240		
DB	181	ARLWYVDAFMKTAENYAGCAVYIINDEADALGPGYGEFDIPLITAKYVADG 240		
QY	241	TLRSTEGEDDLMGDVIVHNGOPPELVNVPKRYRFRFLNAASRAWLIVRTSPNVR 300		
DB	241	TLRSTEGEDDLMGDVIVHNGOPPELVNVPKRYRFRFLNAASRAWLIVRTSPNVR 300		

Db 241 TLRSTEGEDODLMDGDIHVNGQPMPELVNQPCKYRFRFLNAVSRAMLIVLRITSSPNVR 300
QY IPFOVIASDAGLLQAPVOTSNLXYLAVEREYIIIDFTNFAQOTLDLRVAETINDVGDDE 360
Db 301 IPFOVIASDAGLLQAPVOTSNLXYLAVEREYIIIDFTNFAQOTLDLRVAETINDVGDDE 360
QY 361 YARLEVMRFVYSSGTVEDNSQVSTLRDVPFPPEKBPADKHFEERSNGHYLINDVGF 420
Db 361 YARLEVMRFVYSSGTVEDNSQVSTLRDVPFPPEKBPADKHFEERSNGHYLINDVGF 420
QY 421 ADVNERVLAKPELGVEWELENSGSGSHVPHILVDKILKRTGGQVMPYESAGLK 480
Db 421 ADVNERVLAKPELGVEWELENSGSGSHVPHILVDKILKRTGGQVMPYESAGLK 480
QY 481 DVVNLGREGETLTIEAHYOPMTGAYWMHCHNLIHEDNDMAAVFNTVAMEEKGYLODEPBDP 540
Db 481 DVVNLGREGETLTIEAHYOPMTGAYWMHCHNLIHEDNDMAAVFNTVAMEEKGYLODEPBDP 540

541 MNPKRAVPYRNNDPHARAGNFSASITARVOELAEQEPYRNRLDEILDIGIEE 594
541 MNPKRAVPYRNNDPHARAGNFSASITARVOELAEQEPYRNRLDEILDIGIEE 594

RESULT 2

US-10-080-210-2
; Sequence 2, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/720,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Stachybotrys chartarum
US-10-080-210-2

Query Match 100.0%; Score 3189; DB 12; Length 594;

Best Local Similarity 100.0%; Pred. No. 2.6e-251; Mismatches 0; Indels 0; Gaps 0;

Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLFMSWOLAAASGLISGLVIGIPMDGSHPIEAVDPEVTEVFADSLAAAGDDWESPXY 60
QY 61 MLFMSWOLAAASGLISGLVIGIPMDGSHPIEAVDPEVTEVFADSLAAAGDDWESPXY 60
Db 61 MLFMSWOLAAASGLISGLVIGIPMDGSHPIEAVDPEVTEVFADSLAAAGDDWESPXY 60
QY 61 NLLYRNALPIPPVKOPKMIITNPVTGKDITWYEIEIKFQOIRIYPTLRPATLVGDGKSP 120
Db 61 NLLYRNALPIPPVKOPKMIITNPVTGKDITWYEIEIKFQOIRIYPTLRPATLVGDGKSP 120
QY 61 NLLYRNALPIPPVKOPKMIITNPVTGKDITWYEIEIKFQOIRIYPTLRPATLVGDGKSP 120
Db 61 NLLYRNALPIPPVKOPKMIITNPVTGKDITWYEIEIKFQOIRIYPTLRPATLVGDGKSP 120
QY 121 GPTFNVPRGTEVYVRFINNATVENSVHLHGSFSPRAFDGMAEDVTFPGKYDYFFPNYOS 180
Db 121 GPTFNVPRGTEVYVRFINNATVENSVHLHGSFSPRAFDGMAEDVTFPGKYDYFFPNYOS 180
QY 121 GPTFNVPRGTEVYVRFINNATVENSVHLHGSFSPRAFDGMAEDVTFPGKYDYFFPNYOS 180
Db 121 GPTFNVPRGTEVYVRFINNATVENSVHLHGSFSPRAFDGMAEDVTFPGKYDYFFPNYOS 180
QY 181 ARLLMYHDHAFMKTAENAYFGQAGAYIINDAEADALGIPSGYGEEDIPLLITAKYYNADG 240
Db 181 ARLLMYHDHAFMKTAENAYFGQAGAYIINDAEADALGIPSGYGEEDIPLLITAKYYNADG 240
QY 181 ARLLMYHDHAFMKTAENAYFGQAGAYIINDAEADALGIPSGYGEEDIPLLITAKYYNADG 240
Db 181 ARLLMYHDHAFMKTAENAYFGQAGAYIINDAEADALGIPSGYGEEDIPLLITAKYYNADG 240
QY 241 TLRSTEGEDODLMDGDIHVNGQPMPELVNQPCKYRFRFLNAVSRAMLIVLRITSSPNVR 300
Db 241 TLRSTEGEDODLMDGDIHVNGQPMPELVNQPCKYRFRFLNAVSRAMLIVLRITSSPNVR 300
QY 241 TLRSTEGEDODLMDGDIHVNGQPMPELVNQPCKYRFRFLNAVSRAMLIVLRITSSPNVR 300
Db 241 TLRSTEGEDODLMDGDIHVNGQPMPELVNQPCKYRFRFLNAVSRAMLIVLRITSSPNVR 300
QY 301 IPFOVIASDAGLLQAPVOTSNLXYLAVEREYIIIDFTNFAQOTLDLRVAETINDVGDDE 360
Db 301 IPFOVIASDAGLLQAPVOTSNLXYLAVEREYIIIDFTNFAQOTLDLRVAETINDVGDDE 360

QY 361 YARLEVMRFVYSSGTVEDNSQVSTLRDVPFPPEKBPADKHFEERSNGHYLINDVGF 420
Db 361 YARLEVMRFVYSSGTVEDNSQVSTLRDVPFPPEKBPADKHFEERSNGHYLINDVGF 420
QY 421 ADVNERVLAKPELGVEWELENSGSGSHVPHILVDKILKRTGGQVMPYESAGLK 480
Db 421 ADVNERVLAKPELGVEWELENSGSGSHVPHILVDKILKRTGGQVMPYESAGLK 480
QY 481 DVVNLGREGETLTIEAHYOPMTGAYWMHCHNLIHEDNDMAAVFNTVAMEEKGYLODEPBDP 540
Db 481 DVVNLGREGETLTIEAHYOPMTGAYWMHCHNLIHEDNDMAAVFNTVAMEEKGYLODEPBDP 540

RESULT 3

US-10-080-233-2
; Sequence 2, Application US/10080233
; Patent No. US20020151450A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: No. US20020151450A1 Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/10/080,233
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Stachybotrys sp.
US-10-080-233-2

Query Match 100.0%; Score 3189; DB 12; Length 594;

Best Local Similarity 100.0%; Pred. No. 2.6e-251; Mismatches 0; Indels 0; Gaps 0;

Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLFMSWOLAAASGLISGLVIGIPMDGSHPIEAVDPEVTEVFADSLAAAGDDWESPXY 60
Db 1 MLFMSWOLAAASGLISGLVIGIPMDGSHPIEAVDPEVTEVFADSLAAAGDDWESPXY 60
QY 61 NLLYRNALPIPPVKOPKMIITNPVTGKDITWYEIEIKFQOIRIYPTLRPATLVGDGKSP 120
Db 61 NLLYRNALPIPPVKOPKMIITNPVTGKDITWYEIEIKFQOIRIYPTLRPATLVGDGKSP 120
QY 61 NLLYRNALPIPPVKOPKMIITNPVTGKDITWYEIEIKFQOIRIYPTLRPATLVGDGKSP 120
Db 61 NLLYRNALPIPPVKOPKMIITNPVTGKDITWYEIEIKFQOIRIYPTLRPATLVGDGKSP 120
QY 121 GPTFNVPRGTEVYVRFINNATVENSVHLHGSFSPRAFDGMAEDVTFPGKYDYFFPNYOS 180
Db 121 GPTFNVPRGTEVYVRFINNATVENSVHLHGSFSPRAFDGMAEDVTFPGKYDYFFPNYOS 180
QY 121 GPTFNVPRGTEVYVRFINNATVENSVHLHGSFSPRAFDGMAEDVTFPGKYDYFFPNYOS 180
Db 121 GPTFNVPRGTEVYVRFINNATVENSVHLHGSFSPRAFDGMAEDVTFPGKYDYFFPNYOS 180
QY 181 ARLLMYHDHAFMKTAENAYFGQAGAYIINDAEADALGIPSGYGEEDIPLLITAKYYNADG 240
Db 181 ARLLMYHDHAFMKTAENAYFGQAGAYIINDAEADALGIPSGYGEEDIPLLITAKYYNADG 240
QY 181 ARLLMYHDHAFMKTAENAYFGQAGAYIINDAEADALGIPSGYGEEDIPLLITAKYYNADG 240
Db 181 ARLLMYHDHAFMKTAENAYFGQAGAYIINDAEADALGIPSGYGEEDIPLLITAKYYNADG 240
QY 241 TLRSTEGEDODLMDGDIHVNGQPMPELVNQPCKYRFRFLNAVSRAMLIVLRITSSPNVR 300
Db 241 TLRSTEGEDODLMDGDIHVNGQPMPELVNQPCKYRFRFLNAVSRAMLIVLRITSSPNVR 300
QY 241 TLRSTEGEDODLMDGDIHVNGQPMPELVNQPCKYRFRFLNAVSRAMLIVLRITSSPNVR 300
Db 241 TLRSTEGEDODLMDGDIHVNGQPMPELVNQPCKYRFRFLNAVSRAMLIVLRITSSPNVR 300
QY 301 IPFOVIASDAGLLQAPVOTSNLXYLAVEREYIIIDFTNFAQOTLDLRVAETINDVGDDE 360
Db 301 IPFOVIASDAGLLQAPVOTSNLXYLAVEREYIIIDFTNFAQOTLDLRVAETINDVGDDE 360
QY 361 YARLEVMRFVYSSGTVEDNSQVSTLRDVPFPPEKBPADKHFEERSNGHYLINDVGF 420
Db 361 YARLEVMRFVYSSGTVEDNSQVSTLRDVPFPPEKBPADKHFEERSNGHYLINDVGF 420
QY 421 ADVNERVLAKPELGVEWELENSGSGSHVPHILVDKILKRTGGQVMPYESAGLK 480
Db 421 ADVNERVLAKPELGVEWELENSGSGSHVPHILVDKILKRTGGQVMPYESAGLK 480
QY 481 DVVNLGREGETLTIEAHYOPMTGAYWMHCHNLIHEDNDMAAVFNTVAMEEKGYLODEPBDP 540
Db 481 DVVNLGREGETLTIEAHYOPMTGAYWMHCHNLIHEDNDMAAVFNTVAMEEKGYLODEPBDP 540

Db 481 DVVWLGREGTLLTEAHQPTWGAYMHCNLIHEDNDMAVFNVTAMEKGLODFEDP 540
Oy 541 MNPWRVAVPNRNFHARAGNFSAESTARVOELAEOPRYRLDEILDLIGEE 594
Db 541 MNPWRVAVPNRNFHARAGNFSAESTARVOELAEOPRYRLDEILDLIGEE 594
RESULT 4
US-09-338-723A-4
; Sequence 4, Application US/09338723A
; Patent No. US2002019038A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Wang
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-2
; CURRENT APPLICATION NUMBER: US/09/338, 723A
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220, 871
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 627
; TYPE: PRF
; ORGANISM: Bipolaris spicifera
US-09-338-723A-4
Query Match 61.3%; Score 1954.5; DB 10; Length 627;
Best Local Similarity 61.1%; Pred. No. 9e-151;
Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8;
Oy 2 LFKSMOLAAAGSLGVLGIPMDTSGHPTEAVDEPKTEVPADSLAAAGD----- 53
Db 6 LFSALQLVLS--IAKGIYVAL--SERPAKEVDNTPDEKAA--LASIYEDDPADVYNNL 58
Oy 54 -DMESPYNLLRYNALPIPPVQPKMITNPVTGKDIWYEEIEIKPQORITPTLRPATL 112
Db 59 KMQSPREYLIIRPLRPIPAKEPNK-LTNPTNKEIYELVYIKFQOYVPSLRAPRL 117
Oy 113 VGTGMSGPTPTNPRGTETVYRFINATVENSVHLGSPSRAPFDGMAEDVTFPEKXD 172
Db 118 VGTGDISPPTIIVRGTEAVVRFINOGDRESSIHLGSPSRAPFDGMAEDVIMKGEYD 177
Oy 173 YFEPNVSARLLMYHDHAFMKTAENYFGAGAYIINDAEADALGSPGGEFDPLILT 232
Db 178 YFEPNVSARLLMYHDHAFMKTAENYFGAGAYIINDAEADALGSPGGEYDPLVLS 237
Oy 233 AKYVADGTLRSTEGEDODLMDGVIVHNGQMPFLNVOPRKYRFRFLNAASRAWLLYLV 292
Db 238 SKYVADGTLKTSVGEDEKSVMGDIIVHNGQMPFLNVOPRKYRFRFLNAASRAWLLYLV 297
Oy 293 RTSSPNVRIPFOVIASDAGLLQAPVQTSNLYLAERYEIIIDFTNFAQOTLDLRVAET 352
Db 298 KQDNTATRLPFOVIASDAGLLTHPVQTSMDYVAAERYEIVDFAPYAGQOTLDLRNFAKA 357
Oy 353 NDVGDEDEXTARTLEVYRFFVSSGTVEDNSOVSTLRDVPFRPKSGPADKHFEERSNGH 412
Db 358 NGIGTDDYANTDVKARFHVSSQTVYDNSVVPBQLSQIOFPADKT-DIDHHRFRHTNKE 416
Oy 413 YLINDVGFADYNERVLAKEPLGTVEVWELNENSGGSHPHVHLVDKFLIKRTGGRGO-- 470
Db 417 WRINGIGFADYENRVLAKEPRGTVEVWELNENSGGSHPHVHLVDKFLIKRTGGRGO-- 476
Oy 471 VMPYSAGLKDYVWLGREGTLLTEAHQPTWGAYMHCNLIHEDNDMAVFNVTAMEEK 530
Db 477 VMPYEAAGLKDYVWLGREGTLLTEAHQPTWGAYMHCNLIHEDNDMAVFNVTAMEEK 536
Oy 531 GYLO-EDFEDPMNPKWRAVYPNNDHARAGNFSAESTARVOELAEOPRYRLDEILED 589
Db 537 GYNETTDHDEPDPKWSARPTAGDLTRASGIFSEESIRARVNEALAEOPYSELAAQVYAS 596
Oy 590 L 590

Db 597 L 597
RESULT 5
US-10-080-210-4
; Sequence 4, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huang
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080, 210
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220, 871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338, 723
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 627
; TYPE: PRF
; ORGANISM: Bipolaris spicifera
US-10-080-210-4
Query Match 61.3%; Score 1954.5; DB 12; Length 627;
Best Local Similarity 61.1%; Pred. No. 9e-151;
Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8;
Oy 2 LFKSMOLAAAGSLGVLGIPMDTSGHPTEAVDEPKTEVPADSLAAAGD----- 53
Db 6 LFSALQLVLS--IAKGIYVAL--SERPAKEVDNTPDEKAA--LASIYEDDPADVYNNL 58
Oy 54 -DMESPYNLLRYNALPIPPVQPKMITNPVTGKDIWYEEIEIKPQORITPTLRPATL 112
Db 59 KMQSPREYLIIRPLRPIPAKEPNK-LTNPTNKEIYELVYIKFQOYVPSLRAPRL 117
Oy 113 VGTGMSGPTPTNPRGTETVYRFINATVENSVHLGSPSRAPFDGMAEDVTFPEKXD 172
Db 118 VGTGDISPPTIIVRGTEAVVRFINOGDRESSIHLGSPSRAPFDGMAEDVIMKGEYD 177
Oy 173 YFEPNVSARLLMYHDHAFMKTAENYFGAGAYIINDAEADALGSPGGEFDPLILT 232
Db 178 YFEPNVSARLLMYHDHAFMKTAENYFGAGAYIINDAEADALGSPGGEYDPLVLS 237
Oy 233 AKYVADGTLRSTEGEDODLMDGVIVHNGQMPFLNVOPRKYRFRFLNAASRAWLLYLV 292
Db 238 SKYVADGTLKTSVGEDEKSVMGDIIVHNGQMPFLNVOPRKYRFRFLNAASRAWLLYLV 297
Oy 293 RTSSPNVRIPFOVIASDAGLLQAPVQTSNLYLAERYEIIIDFTNFAQOTLDLRVAET 352
Db 298 KQDNTATRLPFOVIASDAGLLTHPVQTSMDYVAAERYEIVDFAPYAGQOTLDLRNFAKA 357
Oy 353 NDVGDEDEXTARTLEVYRFFVSSGTVEDNSOVSTLRDVPFRPKSGPADKHFEERSNGH 412
Db 358 NGIGTDDYANTDVKARFHVSSQTVYDNSVVPBQLSQIOFPADKT-DIDHHRFRHTNKE 416
Oy 413 YLINDVGFADYNERVLAKEPLGTVEVWELNENSGGSHPHVHLVDKFLIKRTGGRGO-- 470
Db 417 WRINGIGFADYENRVLAKEPRGTVEVWELNENSGGSHPHVHLVDKFLIKRTGGRGO-- 476
Oy 471 VMPYSAGLKDYVWLGREGTLLTEAHQPTWGAYMHCNLIHEDNDMAVFNVTAMEEK 530
Db 477 VMPYEAAGLKDYVWLGREGTLLTEAHQPTWGAYMHCNLIHEDNDMAVFNVTAMEEK 536
Oy 531 GYLO-EDFEDPMNPKWRAVYPNNDHARAGNFSAESTARVOELAEOPRYRLDEILED 589
Db 537 GYNETTDHDEPDPKWSARPTAGDLTRASGIFSEESIRARVNEALAEOPYSELAAQVYAS 596
Oy 590 L 590

Db 597 L 597

RESULT 6
US-10-080-210-7
; Sequence 7, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
EO ID NO 7
LENGTH: 627
TYPE: PRT
; ORGANISM: Curvularia pallenscens
US-10-080-210-7

Query Match 60.5%, Score 1929.5; DB 12; Length 627;
Best Local Similarity 60.5%, Pred. No. 9.7e-149;
Matches 364; Conservative 81; Mismatches 134; Indels 23; Gaps 9;

2 LFKSMOLAAASGLSGVIGIPMDGSHIEAVDEPVKTEVADSLAAGD----- 53
6 LFSALQALAS--LAKGIVGAL--SERPAKIDETPDEKAA--LAAIVEDPADVERIL 58
54 -DMSPRYNLRYNALPIPVKOPKMITNPVTGKDIWYIEIEIKFQORITPLRPATL 112
59 KDMSPREPLIFREALPIPAKEPNK-MTNPTNKEIMYIEIVIKFQOYVPSLRARL 117
113 VGYGMSGPFTFNPRTGTEYVRFINNAVENSVAHLGSPSRAPDGAEDVTPGCKYD 172
118 VGYGMSGPFTIYVPRGTEAVRVNNOGDRSSIHLSGSPSRAPDGAEDLIMKGPCKD 177
173 YFPNYSARLLWYHDAFMKTAENAVFGAGATYIINDEADALGPSGGEFDIPLLT 232
178 YYYNNNAARLWYHDAFMKTAENAVFGAGATYIINDEADALGPSGGEFDIPLLT 237
233 AKYNNADGTLRSTEGEDQDLMDVYIHVNGOPWPLNVOPRKYRFRFLNAAVSRAMLTYL 292
238 SKFYNSDGTLOTSGEDNSLMDVYIHVNGOPWPLNVOPRKYRFRFLNAAVSRAMPALTYF 297
293 RTSSPNVRIPPOVYASAGLLQAPVOTSNLYLAVEREITIDTFNFRAGOTLDLRNVAET 352
298 KOQATATRLPPOVYASAGLLQAPVOTSNLYLAVEREITIDTFNFRAGOTLDLRNVAET 357
353 NDVDEDEYARTLEVMRFVSSGTVEDNSOVPTLRDVPKPKRGPADKHKFKERSNGH 412
358 NGVETDDDYANTDKVMRFVSSGTVEDNSOVPTLRDVPKPKRGPADKHKFKERSNGH 416
413 YLINDVGFADVNERVYAKPELGTVEVWELNENSGGWSHPVHILVDFEILKRTGG--RG 469
417 WRINGISGFADYONRILAKVPRGVEWELNENSGGWSHPVHILVDFEIVARYYDESRG 476
470 QWMPYESAGLKDVYVLRGGETITTEAHYQPTGAYMMHCHNLIHEDNDMAAVNTAAEE 529
477 -VMYESAGLKDVYVLRGGETITTEAHYQPTGAYMMHCHNLIHEDNDMAAVNTAAEE 535
530 KGYLQ--EDFEDPMNPKRAVYNNRNDHARAGNSASITARVOELAEQBYNLDLELE 588
536 FGINETTFDHPEDSRMSARPEFTADLTARSGITSEASIRARVNLAEQBYSELAQVTA 595
589 DL 590
596 SL 597

RESULT 7
US-09-942-185-4
; Sequence 4, Application US/09942185
; Patent No. US20020165113A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Convents, Daniel
; APPLICANT: Doornink, Monique
; APPLICANT: van Gastel, Frans
; APPLICANT: Rodrigues, Ana
; APPLICANT: Topozada, Amr
; APPLICANT: De Vries, Cornelis Hendrikus
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: Detergent Compositions Comprising No. US20020165113A1 Phenol
; FILE REFERENCE: C7567
; CURRENT APPLICATION NUMBER: US/09/942,185
; CURRENT FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
LENGTH: 572
TYPE: PRT
; ORGANISM: Myrothecium verucaria
US-09-942-185-4

Query Match 54.1%, Score 1724.5; DB 9; Length 572;
Best Local Similarity 60.3%, Pred. No. 4.2e-132;
Matches 322; Conservative 75; Mismatches 128; Indels 9; Gaps 7;

57 SPYNLRYNALPIPVKOPKMITNPVTGKDIWYIEIEIKFQORITPLRPATLVGYD 116
43 SPQYR-METVPLRPVQVPRRLVTNPNNGEIMYIEIEIKFQOYVPSLRARL 101
117 GMSGPFTFNPRTGTEYVRFINNAVENSVAHLGSPSRAPDGAEDVTPGCKYD 176
102 GMSGPFTFNPRTGTEYVRFINNAVENSVAHLGSPSRAPDGAEDVTPGCKYD 161
177 NYGSRLLWYHDAFMKTAENAVFGAGATYIINDEADALGPSGGEFDIPLLTAKY 236
162 NRQSRLLWYHDAFMKTAENAVFGAGATYIINDEADALGPSGGEFDIPLLTAKY 221
237 NADGTLSTEGEDQDLMDVYIHVNGOPWPLNVOPRKYRFRFLNAAVSRAMLTYL 296
222 TANGLVYTTNGLNLSFMDVYIHVNGOPWPLNVOPRKYRFRFLNAAVSRAMPALTYF 281
297 PNVRIPPOVYASAGLLQAPVOTSNLYLAVEREITIDTFNFRAGOTLDLRNVAET 355
282 IDTRLPKRYIASDSGLLEHPRADTSLIYMAERIEVYFDSYAGKTIELRNLGSGIGI 341
356 GDEDEYARTLEVMRFVSSGTVEDNSOVPTLRDVPKPKRGPADKHKFKERSNGH 413
342 GTDYDDYNTDKVMRFVSSGTVEDNSOVPTLRDVPKPKRGPADKHKFKERSNGH 399
414 LINDVGFADVNERVYAKPELGTVEVWELNENSGGWSHPVHILVDFEILKRTGG--QV 471
400 TINGVADADYONRILAKVPRGVEWELNENSGGWSHPVHILVDFEIVARYYDESRG 459
472 MPYSSAGLKDVYVLRGGETITTEAHYQPTGAYMMHCHNLIHEDNDMAAVNTAAEE 531
460 MPYSSAGLKDVYVLRGGETITTEAHYQPTGAYMMHCHNLIHEDNDMAAVNTAAEE 518
532 YLQDEDFEDPMNPKRAVYNNRNDHARAGNSASITARVOELAEQBYNLDLELE 585
519 YNATVYDPMKELMQRARPELGEFQAGSGQSVQAVYERIQTMAYEYRYAADE 572

RESULT 8
US-09-942-185-2
; Sequence 2, Application US/09942185
; Patent No. US20020165113A1
; GENERAL INFORMATION:

Query Match	53.8%;	Score 1716.5;	DB 9;	Length 583;
Best Local Similarity	61.0%;	Pred. No. 1.9e-131;		
Matches 330;	Conservative 67;	Mismatches 125;	Indels 19;	Gaps 9;

[illegible]

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OM protein - protein search, using sw model

Run on: July 1, 2003, 10:37:11 ; Search time 43 Seconds
(without alignments)
1327.996 Million cell updates/sec

Title: US-10-080-233-2
Perfect score: 3189
Sequence: 1 MFKSMQLAASGLSLGVLG.....AEQEPYNRDEILEDIGIEE 594

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1724.5	54.1	572	2	B48521
2	713	27.4	513	2	F69604
3	480	15.1	568	2	B86364
4	450	14.1	521	2	G96734
5	439.5	13.8	527	2	C70397
6	405.5	12.6	533	2	AC0414
7	402	12.6	494	2	AC3582
8	391	12.3	536	2	AF0523
9	388.5	12.2	516	2	C64735
10	385.5	12.1	516	2	G90644
11	385.5	12.1	516	2	G85495
12	340.5	10.7	470	2	G65088
13	335.5	10.5	470	2	E91116
14	335.5	10.5	470	2	E85961
15	323.5	10.1	470	2	AD0888
16	315.5	9.9	513	2	G81298
17	303	8.9	474	2	AD0083
18	284	8.9	1662	2	T18540
19	241	7.6	311	2	H64157
20	231.5	7.3	570	2	H83368
21	223	7.0	500	2	H83910
22	216.5	6.8	463	2	G83175
23	215.5	6.8	611	2	C82845
24	214	6.7	721	2	H82528
25	195.5	6.1	632	2	F83387
26	192	6.0	609	1	KSPSCY
27	190.5	6.0	529	2	S68120
28	189.5	5.9	635	2	A36868
29	188.5	5.9	520	2	S59533

206 is cut off

close

ALIGNMENTS

30	188.5	5.9	520	2	JC5356	laccase (EC 1.10.3
31	187.5	5.9	504	2	F70813	hypothetical prote
32	185	5.8	527	2	JC5357	laccase (EC 1.10.3
33	184.5	5.8	573	2	T02743	laccase (EC 1.10.3
34	183	5.7	619	1	KSNCLT	laccase (EC 1.10.3
35	180	5.6	533	2	S62371	laccase (EC 1.10.3
36	180	5.6	621	2	S72493	laccase (EC 1.10.3
37	179.5	5.6	605	2	S52253	copper resistance
38	179	5.6	548	2	S18746	laccase (EC 1.10.3
39	176	5.5	551	2	T02752	probable laccase (
40	176	5.5	619	1	KSNCLT	laccase (EC 1.10.3
41	172.5	5.4	520	2	A35883	laccase (EC 1.10.3
42	172.5	5.4	520	2	B35883	ligninolytic pheno
43	171.5	5.4	552	2	A51027	L-ascorbate oxidas
44	169.5	5.3	579	2	S11027	L-ascorbate oxidas
45	167	5.2	512	2	JC5355	laccase (EC 1.10.3

RESULT 1

B48521
bilirubin oxidase (EC 1.3.3.5) - fungus (Myrothecium verrucaria)
C:Species: Myrothecium verrucaria
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C/Accession: B48521; A48521
R:Koike, S.; Ando, K.; Kaji, H.; Inoue, T.; Muro, S.; Takeuchi, K.; Samejima, T.
J. Biol. Chem. 268, 18801-18809, 1993
A>Title: Molecular cloning of the gene for bilirubin oxidase from Myrothecium verruca
A/Reference number: A48521; MIMD:9336794; PMID:8360171
A/Accession: B48521
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-572 <KOI1>
A:Cross-references: GB:D14081; NID:9436236; PIDN:BA03166.1; PID:9456710
A/Note: sequence extracted from NCBI backbone (NCBIN:136730, NCBI:P.136732)
A/Accession: A48521
A/Status: preliminary
A/Molecule type: mRNA; protein
A/Residues: 1-572 <KOI2>
A:Cross-references: GB:D14081; NID:9436236; PIDN:BA03166.1; PID:9456710
A/Note: sequence extracted from NCBI backbone (NCBIN:136728, NCBI:P.136729)
C/Keywords: oxidoreductase

Query Match 54.1% Score 1724.5; DB 2; Length 572;

Best Local Similarity 60.3%; Pred. No. 1.4e-123;

Matches 322; Conservative 75; Mismatches 128; Indels 9; Gaps 7;

OY	57	SPRYNLRYNALPPIPVKOKMITNPVTKDIWYIEIKPQORIPYPLRPAATVGYD	116
OY	43	SPQYP-MFTVPDIPVYKQRLVTPVNGOEIWTYEVELEKPTTHOYPLDGLADLVGID	101
OY	117	GMSPGPTFVNPQCTETVVRINNATVENSYHLGSPSRAPFDGMADVTFPGYKDYYP	176
OY	102	GMSPGPTFVNPQCTETVVRINNATVENSYHLGSPSRAPFDGMADVTFPGYKDYYP	161
OY	177	NYOSARLWYHDAFPAKTYENAYFGGAYIINDERDALGPPSGEEDIPILITAKYI	236
OY	162	NROSARTLWYHDAFPAKTYENAYFGGAYIINDERDALGPPSGEEDIPILITAKYI	221
OY	237	NMGCTLRSTEGEODLAGDVIHYNGOPWPLNQPARKYRFRPLDAVSRSGFYADDTDA	296
OY	222	TANGNLVTNNGELNSTWGDVHYNGOPWPKYRFRPLDAVSRSGFYADDTDA	281
OY	297	PVNRIPFOYIASDAGLLQAPVQTSNLYLAVEREYIITDFTNAGOTLDLRYN-AETNDV	355
OY	282	IDRLRPFYIASDAGLLQAPVQTSNLYLAVEREYIITDFTNAGOTLDLRYN-AETNDV	341
OY	356	GDEDEYARLEWRFVYSSGYE-DNSQVPSITRDVFP-PKKEGADYHFKERNGHY	413
OY	342	GDYTDYNDYKWARFVYADDTTOPDTSVVPANLRDVPFSPPTNTNP--ROFRGRGPTW	399

Db 249 IHPQMPYEGDYIIVNGKAMPRLNRRKRYRRIINASNAREFFKFF-----SNGLDF 302
OY 304 QVVASAGLLQAPVQTSNLYLAVEREIIIDFTNAGQPLDLRNA-----ETNDYGD 358
Db 303 IIVGSSAYLSKSPKWKRSILSPSEIVDVVDFKSPSRVLANDPYPSGDPPNEE 362
OY 359 DEYARILEVRFVYSGTVEDNSQVSTLRDVPFPKRGADKHEFER--SNG-----H 412
Db 363 NG-----KVMKFIINNESEDCTIPKRLINPNADVSNVLRYSIMRYEVSNDDEPT 417
OY 413 YLINDYGF-ADVNERVLAKPELGTVEWELENSSGSHPHVHLVDFKILKRTGGRQV 471
Db 418 LTVNGLPYEPAYTE-----FKSGSTVEWEVINTLED-NHPLHILGLFKVEQTA----- 467
OY 472 MPYESAGLKD-----VWMLRGSETLITIAHYQPMTG----- 502
468 --LLAAGLEEFKECKMTKQNDAYKQISKYARGKATATAEHRKMKVFKMPPGHVTRILV 525
503 -----AYMWHCHNLIEDNDMAVFN 524
526 RESYIHTNMSYPPDPYQOEYGVYHCHLHDHEDMMMRPLKV 566

RESULT 4
G96734

Spore coat protein-like protein, 24980-21957 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G96734
R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maltl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: G96734
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-591 <STO>
A:Cross-references: GB:AE005173; NID:g67141313; PIDN:AAF26006.1; GSFD:GN00141
C:Genetics:
Gene: F23N20.3
Map position: 1

Query Match 14.1%; Score 450; DB 2; Length 591;

Best Local Similarity 27.4%; Pred. No. 2.9e-26;
Matches 142; Conservative 74; Mismatches 182; Indels 120; Gaps 18;

OY 109 PATLVGYDMS-----PGFTFNVPRGTETVVFVN-----NATV 142
Db 86 PAFPVAYGTSKSKSATVPPTIEAVYGVDTYVWRNMLPLHLHPDPTSPALPKKGI 145
OY 143 ENSVHLHSGSPSRAPFGMAEDVTFPGKYD-----YFPNTQSARLLMTHDAFMK 193
Db 146 PTVVHLHGGIHEPTSDGNA-DSWFTAGFKETGSKWKTKTTHAYVKKOOPGMWVHDAAGL 204
OY 194 TAENAYFGAGAYII-NDKEDALGLPSGGEEDIPILITAKYYNMDGTL-RSTEGED-- 249
Db 205 TRVNLALAGLGSITILHSSVESPLRLPTG-REFDRPLVITDRSFRKDGSTYMANATGNNPT 263
OY 250 -----ODLMGDVYHVGQWPPLNQPRTKRYRFLNAASRAMLYLVVTSPPNVAIFP 303
Db 264 IHPQMPYEGDYIIVNGKAMPRLNRRKRYRRIINASNAREFFKFF-----SNGLDF 317
OY 304 QVVASAGLLQAPVQTSNLYLAVEREIIIDFTNAGQPLDLRNAETMDVGDDEYAR 363
Db 318 IIVGSSAYLSKSPKWKRSILSPSEIVDVVDFKSPSRVLANDPYPSGDPPNEE 377

OY 364 TLEVMRFVSGTVEDNSQVSTLRDVPFPKRGADKHEF--KFEESNG-----HYLIN 416
Db 378 NSKMKRTIYKSSVDTSTIPKLELP-PAHYSTRTTRKIANFEVSSIDETFLYIN 436
OY 417 DYGFADYNERVLAKPELGTVE-----VWELENSSGSHPHVHLVDFKILKRTG 466
Db 437 GLPY--NAVYTERPKIGTSEFKSLMLTIKWEVINTLED-NHPLHILGLFKVLEOTA 492
OY 467 -----GROQVPEASGLKDYV-----W 484
Db 493 LVNSEEFIECKTRKNDAYKCEISKYARGKATATAEHRKMKVFKMPPGHVTRILV 552
OY 485 IGRGETLITIAHYQPMTGAYMWHCHNLIEDNDMAVFN 522
Db 553 IHSNYSIFDAPQEP--GYVHCHLHDHEDMMMRPLKV 587

RESULT 5
C70397

periplasmic cell division protein (SufI) - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1998
C:Accession: C70397
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: C70397
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-527 <NOF>
A:Cross-references: GB:AE000724; NID:g2963585; PIDN:AAC07157.1; PID:g2983586; GB:AE0
A:Experimental source: strain VFS
C:Genetics:
A:Gene: sufI

Query Match 13.8%; Score 439.5; DB 2; Length 527;

Best Local Similarity 30.1%; Pred. No. 1.6e-25;
Matches 147; Conservative 72; Mismatches 191; Indels 79; Gaps 21;

OY 98 PFOQRIYPLRPATLVGYDMS-----GPFTFNVPRGTETVVFVN-----NATV 146
Db 58 PDGGRVSIKAKWTTLVYIPKSTDMLYEIDNEVNPVIFLRKQGFSADEVNNSGDSII 117
OY 147 HLHSGSPSRAP--DGAEDVTFPGKYDYFPNT--QSARLLMTHDAFMKTAENAYFG 201
Db 118 HWHG--FRAPMKSDGHPYVAVKDGE--TYSVPFTIIDRSQTYFHPHPRGQYVYGG 173
OY 202 QACAYIINDKEDAL--GLPSGGEEDIPILITAKYYNMDGTLRSTEGEDDLMGDVYH 259
Db 174 LAGIITIEDDEDKQALDLEGVDIPILIDKTPDSSGQALVYVPMGMRGFWGDTTLV 233
OY 260 NGQWPPLNQPRTKRYRFLNAASRAMLYLVVTSPPNRIPOVVASAGLLQAPVQ 319
Db 234 NLFPNPMDYERKTRIRILNAGSNARVRLALR--CNGRMKRWVYVGGGLDLPYKEV 290
OY 320 SNIYLAVEREIIIDFT-----NFAQOTLDL-----RNAETN--- 353
Db 291 NEIIVAGGERIDILVDFRDSVNDVYIKLYNPHILIGMIGMRGMRGOMGNGMN 350
OY 354 -DVG--DEDYARILEVRFVYSGTVEDNSQVSTLRDVPFPKRGADKHEFER-- 410
Db 351 MDGMKADNSEF--EVMFRVTKDSAYDS-TPQRLSEVT-PLNTGADVOYRTLMRR 404
OY 411 GHYLIN-----DVGA--RVYLAKEPELGTVEWELENSSGSHPHVHLVDFKIL 462
Db 405 IAVTINTEWEDGAYANQDINNPKVLEQNGNDVILIEVYNNIGM--HNNHNGFOYOL 463
OY 463 KRTGGRQVMPYESA--GLKDYVWLGKGEFLTE--AHYQPMTGAYMWHCHNLIEDND 517
Db 464 ERSIG-----PLRATDGLGMDVYVAVMETVRIADVMSHRYNEHQIYLCHILEHDEG 518

OY 518 MAAVFNVT 526
DB 519 MAAVFNVT 527

RESULT 6

AC0414
Probable exported protein YP03409 [Imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AC0414
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tildall, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11566360
A:Accession: AC0414
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-533 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC92639.1; PID:g15981336; GSPDB:GN00175
A:Gene: YP03409

Query Match 12.7%; Score 405.5; DB 2; Length 533;
Best Local Similarity 27.1%; Pred. No. 6.2e-23;
Matches 146; Conservative 57; Mismatches 217; Indels 119; Gaps 18;

OY 68 LPPIPVKOPK---MITNPVTGKDIWYEIEIKPFOQRITPLRPATLV---GYDMSPG 121
DB 34 LPPIPLDPDANGKINLNIQGSYVWL-----PSTATQTMGYNLIG 76
OY 122 PTFNVPRGTETVVRFINNATVENSYHLGSPSRAPFDGMAEDVTPPEKDYPPNYOSA 181
DB 77 PAIRLQRGKAVYIDITNLPEATYVHMGLIEIGVDGQALIQGAKROYTFVQEP 136
OY 182 RLWVHDAFMKTAENAFGQAGATYINDEADALGLPSGGEFPIPLITAKTYNADCT 241
DB 137 ATCWHPRHTSKTGQVAMGLGLVLLIDSDSETPLPRQMGVDDIPYIADKLDKHQ 196
OY 242 LRSFGEODL-----MGDVHVGQPPWPFVNOVPRKY-RPRPLNAASRAMLYL 291
DB 197 V-----DYOLDVMTAAVGMFEDRMILNCGVPR-OQITPRGWRLRLNCGNARSLNLA 249
OY 292 VRTSSPNVRIPFOVIASDAGLQAPVQTSNLYLAVEREIIIDTFNAGOTLDRVAE 351
DB 250 -----SDGRPMYVIASDGLLAEPVVRRELPLMGERPEVLVDTRD--GQSLDLVTLPV 301
OY 352 TNDVODEDEYARTLEVMRFVYSSGIVEDNSQV-PESTLDVPPPPHKEGRADKHF----- 404
DB 302 TOMGNTLAPFDQPLFLRIQPS--LAIGSOVLPESLVVIPELADVTGVOERWFOIMDP 358
OY 405 KEERSNGHYLI-----NDVGFAD----- 422
DB 359 KIDMIGMQLAVARYGMKAMGMNHNHGMGMDHGNRPDMSCGKKKMGDHTGACAPAFN 418
OY 423 -----VNERVLAKE-----LGTVEVWELENSGSHPHYHLVDFKILKRTGKQ 470
DB 419 FSHNRINGKAFSMTEPAFPAKQKQYKWTISGEGDMLHPRHVHGTOFRILTEG---- 474
OY 471 VMPE-SAGLKDVMVL--GRGETLTIEAHYQPTGAYVMHCHNLIHEDNDMAVFNVT 526
DB 475 KPPAEHRGMWDIVAVEGARSEILVRFNYLAPASTPYMAHCHLHEHEDTGMALGPTVA 533

RESULT 7

AC3582
Probable blue-copper protein yack precursor [Imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: AC3582
R:DelVecchio, V.G.; Kaprat, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova,

; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A:Reference number: AB3252; PMID:11756688

A:Accession: AC3582
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-494 <KUR>
A:Cross-references: GB:AE008918; PIDN:AAL53822.1; PID:g17984756; GSPDB:GN00191
A:Experimental source: strain 16M
A:Genetics:
A:Gene: BME10580
A:Map position: 11

Query Match 12.6%; Score 402; DB 2; Length 494;
Best Local Similarity 26.4%; Pred. No. 1e-22;
Matches 142; Conservative 65; Mismatches 208; Indels 122; Gaps 17;

OY 56 ESPYNNLYRNALPIPVKOPKMITNPVTGKDIWYEIEIKPFOQRITPLRPATLVG 114
DB 7 KAP-----LPLPLVEP-----DASG-----IVRLKVRGRSHFAKGYAASAG 46
OY 115 YDMSGPPFENVPRGTETVVRFINNATVENSYHLGSPSRAPFDGMAEDVTPPEKDYK 174
DB 47 INGAVLGLPLVRLMSEESTLISVENAMDEETILHMGLEVPSSHLDGCPHNVIAFGAKWEK 106
OY 175 PPNYSARLLWYHDAFMKTAENAFGQAGATYINDEADALGLPSGGEFPIPLITAK 234
DB 107 VAVNQPASPMWPHPLHGHTRQAHMGIALMIVBDQDAERGLPETYGVDDPLVLDOR 166
OY 235 YNADGTLRSTEGED-----QDL-----MGDVHVGQPPWPFVNOVPRKYRPRFMAVS 284
DB 167 -----RVIEGDAVYAPDMDLJHGRGDMVLVNGAIAPEARVPAAMVRLRLNGANA 218
OY 285 RAMLYLVRTSSPNRI-----PFOVIASDAGLQAPVQTSNLYLAVEREIIIDTFN 340
DB 219 RNF-----HTRPADGRPLVIASDAGGGLISQPSVLEQTLISPERIEVLVDFSN-- 266
OY 341 GQTLDRNVAETNDVDEDEYARTLEVMRFVYSSGIVEDNSQVPESTLDVPPPPHKEGPA 400
DB 267 GEAVDLVLYGD--NGSGD-----GLHLRFYVDPALLEGVAKPVPVSLDOPAPDEKLSVQ 319
OY 401 DKHFEFR-----SNGHYLVNDFPADV----- 424
DB 330 RRSFEDERMAENMKLNRQPSNPHASGDDMDHHEKSMAGMDHMGSRSAADAGPAL 379
OY 425 -----ERYLAKPELGTVEVWELENSGSHPHYHLVDFKILKRTG 466
DB 380 DALTSGVOMALADKRFDERIDVEAKLSWEIMEL--TSREAHFPHIHGASFRLISNG 437
OY 467 GRGQVPYAESAGLKDVMVL--GRGETLTIEAHYQPTGAYVMHCHNLIHEDNDMAVF 522
DB 438 KK---PRAHQGMKDTALIDGKAEILVHFDREARASHPFMFCHLHEHEDVGMMAOF 491

RESULT 8

AB0523
Probable multicopper oxidase precursor [Imported] - Salmonella enterica subsp. enteri
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AF0523
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
S.; Moulé, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A:Reference number: AB0502; PMID:11677608
A:Accession: AF0523
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-536 <PAR>

Gencode version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2003, 10:33:51 ; Search time 24 Seconds

(without alignments)
1026.539 Million cell updates/sec

Title: US-10-080-233-2

Perfect score: 3189

Sequence: 1 MFKSMQGLAASGLSLGVLC.....AQEPYNRDELLEDGIRE 594

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

rchd: 112892 seqs, 41476328 residues

al number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SWISSPROT 40.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1724.5	54.4	572	1	BRLN_MYRVE
2	713	22.4	513	1	COTR_BACSU
3	519	16.3	642	1	PHSA_STRAT
4	405.5	12.7	533	1	CUBO_YERPE
5	391	12.3	536	1	CUBO_SALTI
6	390	12.2	536	1	CUBO_SALTY
7	388.5	12.2	516	1	CUBO_SALTY
8	385.5	12.1	516	1	CUBO_ECOLI
9	340.5	10.7	470	1	SUPR_ECOLI
10	323.5	10.1	470	1	SUPR_SALTY
11	241	7.6	311	1	SUPR_HAEIN
12	192.5	6.0	520	1	LACI_TRAVI
13	192	6.0	609	1	COPA_PESM
14	190	6.0	527	1	LAC5_TRAVE
15	188.5	5.9	520	1	LAC4_TRAVE
16	188.5	5.9	520	1	LAC4_TRAVE
17	185	5.8	527	1	LAC5_TRAVI
18	180	5.6	533	1	LAC2_PLEOS
19	180	5.6	621	1	LAC2_PODAN
20	179.5	5.6	605	1	PCOA_ECOLI
21	179	5.6	548	1	LAC1_PHLRA
22	177.5	5.6	520	1	LAC2_AGABI
23	177	5.6	619	1	LAC1_NEUCR
24	176.5	5.5	519	1	LAC2_TRAVI
25	176.5	5.5	520	1	LAC1_AGABI
26	176	5.5	619	1	LAC2_NEUCR
27	174	5.5	591	1	LAC1_CRYPA
28	172.5	5.4	520	1	LAC1_CORHI
29	171.5	5.4	552	1	ASO_CUCPM
30	169.5	5.3	519	1	LAC2_TRAVE
31	169.5	5.3	579	1	ASO_CUCMA
32	166.5	5.2	622	1	FET5_YEAST
33	163.5	5.1	624	1	FET3_CANAL

Result ID	Score	Query Match	Length	ID	Description
34	161.5	5.1	531	1	LAC4_THACU
35	160.5	5.0	529	1	LAC1_PLEOS
36	155.5	4.9	608	1	YD56_YEAST
37	155.5	4.9	622	1	YAK8_SCHPO
38	154	4.8	587	1	ASO_CUCSA
39	151.5	4.8	486	1	LAC1_BORCI
40	139.5	4.4	473	1	LAC3_TRAVI
41	135.5	4.2	636	1	FET3_YEAST
42	126.5	4.0	572	1	LAC3_THACU
43	121	3.8	576	1	LAC1_THACU
44	114	3.6	725	1	NCA2_MOUSE
45	114	3.6	1115	1	NCA1_MOUSE

Result ID	Score	Query Match	Length	ID	Description
1	1724.5	54.4	572	1	BRLN_MYRVE
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3	519	16.3	642	1	PHSA_STRAT
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5	391	12.3	536	1	CUBO_SALTI
6	390	12.2	536	1	CUBO_SALTY
7	388.5	12.2	516	1	CUBO_SALTY
8	385.5	12.1	516	1	CUBO_ECOLI
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11	241	7.6	311	1	SUPR_HAEIN
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13	192	6.0	609	1	COPA_PESM
14	190	6.0	527	1	LAC5_TRAVE
15	188.5	5.9	520	1	LAC4_TRAVE
16	188.5	5.9	520	1	LAC4_TRAVE
17	185	5.8	527	1	LAC5_TRAVI
18	180	5.6	533	1	LAC2_PLEOS
19	180	5.6	621	1	LAC2_PODAN
20	179.5	5.6	605	1	PCOA_ECOLI
21	179	5.6	548	1	LAC1_PHLRA
22	177.5	5.6	520	1	LAC2_AGABI
23	177	5.6	619	1	LAC1_NEUCR
24	176.5	5.5	519	1	LAC2_TRAVI
25	176.5	5.5	520	1	LAC1_AGABI
26	176	5.5	619	1	LAC2_NEUCR
27	174	5.5	591	1	LAC1_CRYPA
28	172.5	5.4	520	1	LAC1_CORHI
29	171.5	5.4	552	1	ASO_CUCPM
30	169.5	5.3	519	1	LAC2_TRAVE
31	169.5	5.3	579	1	ASO_CUCMA
32	166.5	5.2	622	1	FET5_YEAST
33	163.5	5.1	624	1	FET3_CANAL

Result ID	Score	Query Match	Length	ID	Description
34	161.5	5.1	531	1	LAC4_THACU
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36	155.5	4.9	608	1	YD56_YEAST
37	155.5	4.9	622	1	YAK8_SCHPO
38	154	4.8	587	1	ASO_CUCSA
39	151.5	4.8	486	1	LAC1_BORCI
40	139.5	4.4	473	1	LAC3_TRAVI
41	135.5	4.2	636	1	FET3_YEAST
42	126.5	4.0	572	1	LAC3_THACU
43	121	3.8	576	1	LAC1_THACU
44	114	3.6	725	1	NCA2_MOUSE
45	114	3.6	1115	1	NCA1_MOUSE

FT METAL 495 495 COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL 496 496 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 500 500 COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL 503 503 COPPER (TYPE 1) (BY SIMILARITY).
 FT CARBOHYD 510 510 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 520 520 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 572 AA: 63947 MW: 5842D6413035E5EF CRC64;
 Query Match 54.1%; Score 1724.5; DB 1; Length 572;
 Best Local Similarity 60.3%; Pred. No. 8.6e-119;
 Matches 322; Conservative 75; Mismatches 128; Indels 9; Gaps 7;
 Oy 57 SPYLLALRNALPFPVQPKMTITNPVTGDIWYELKFPQORITPLPAVLGYD 116
 Db 43 SPQYF-METVLPPIPPVQRLTVNPNVQGEIWEYKFTQVYDGLSADLVGYD 101
 Oy 117 GMSPGPTNPVPGTFTVYRFINNAVENSVHLHSGSPRNPFGMAEDVTFPEYDYEP 176
 Db 102 GMSPGPTNPVPGTFTVYRFINNAVENSVHLHSGSPRNPFGMAEDVTFPEYDYEP 161
 Oy 177 NYQARLLMYHDHAFMKTAENAFEGAGAYIINDAEDALGPSYGERDIPLLITARY 236
 Db 162 NROSARLLMYHDHAFMKTAENAFEGAGAYIINDAEDALGPSYGERDIPLLITARY 221
 Oy 237 NADGTLRSTEGEDDOLMGDVIHVNGQPPFLNVQRRKRRFLNAASRANLLYVTRSS 296
 Db 222 TANGLVLTNGELNSFMDGVIVHNGQPPFKRVKRYRFRLLDAVSRKSLFYPADYDA 281
 Oy 297 PNVRIPFQVYASDAGLLQAPVQTSNLYAVAEYRIIIDFTNFAQOTLDLRNV-AETNDV 355
 Db 282 IDTRLPFKVYASDAGLLQAPVQTSNLYAVAEYRIIIDFTNFAQOTLDLRNV-AETNDV 341
 Oy 356 GDEDEYARTLEVNRVSSGVE-DNSQVPSLTLDVPP-PAKEGPADKHKFKERSNGHY 413
 Db 342 GTDDYDNTDVMRVAADDTPTSVYPAVLRVPPSPPTTNP--ROFRFGRTGPTW 399
 Oy 414 LINDVGFADNVRVLAKEPGLTVEWELNENSSGSHVHILYNDKFLTKRGNG--QV 471
 Db 400 TINGVAPADNVRVLAKEPGLTVEWELNENSSGSHVHILYNDKFLTKRGNG--QV 459
 Oy 472 MPYASAGLKVYVWLGRTETLIEAHYQWPGAYMMHCHNLHEDDMAVFNVTAMEBK 531
 Db 460 MPYASAGLKVYVWLGRTETLIEAHYQWPGAYMMHCHNLHEDDMAVFNVTAMEBK 518
 Oy 532 YLQDEDFEPNPKRAVYNNNDHARAGNSAESTIRAVOELAEQEPYNRIDE 585
 Db 519 YNATVFDPMELMQARPELGEFOAGSOPVQAVERTIQTMAEYRYAADA 572
 LT 2
 -BACSU
 AC P07788; STANDARD; PRT; 513 AA.
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Spore coat protein A.
 GN COTA OR FIG.
 OC Bacillus subtilis.
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RX MEDLINE=97124186; PubMed=8969499;
 RA Boris R., Porwollik S., Schroeter R.;
 RT "The 52 degrees-55 degrees segment of the Bacillus subtilis
 containing the genes cota, gap and gua and the pur gene cluster
 within a 34560 bp nucleotide sequence."
 RL Microbiology 142:3027-3031(1996).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN-168 / Marburg;
 RA MEDLINE=98116660; PubMed=9455482;
 RX Kasahara Y., Nakai S., Ogasawara N., Yata K., Sadate Y.;
 RT "Sequence analysis of the groEST-cota region of the Bacillus subtilis
 genome, containing the restriction/modification system genes."
 RL DNA Res. 4:335-339(1997).
 RN [3]
 RP SEQUENCE OF 1-37 FROM N.A.
 RX MEDLINE=88011308; PubMed=2821284;
 RA Donovan W., Zheng L., Sandman K., Losick R.;
 RT "Genes encoding spore coat polypeptides from Bacillus subtilis."
 RL J. Mol. Biol. 196:1-10(1987).
 RN [4]
 RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=88286730; PubMed=3135411;
 RA Sandman K., Kroos L., Cutting S.M., Youngman P., Losick R.;
 RT "Identification of the promoter for a spore coat protein gene in
 Bacillus subtilis and studies on the regulation of its induction at a
 late stage of sporulation."
 RL J. Mol. Biol. 200:461-473(1988).
 RN [5]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC STRAIN-168;
 RA Wray L.V., Person A.E., Fisher S.H.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN BROWN PIGMENTATION DURING SPOROGENESIS.
 CC -1- SIMILARITY: TO S.ANTIBIOTICUS PHENOXAZINONE SYNTHASE (PNSA).
 CC
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 CC
 CC EMBL: U51115; AAB62305.1; -
 DR EMBL: AB007638; BAA22774.1; ALT_INIT.
 DR EMBL: Z99107; CAB12449.1; -
 DR EMBL: X05678; CAA29165.1; ALT_INIT.
 DR EMBL: X07512; CAA30392.1; -
 DR EMBL: U31756; AAC44642.1; -
 DR PIR: A27393; A27393.
 DR HSSP: P36649; IKV7.
 DR Subtilisin; B610490; cota.
 DR Interpro: IPR001117; Cu-oxidase.
 DR Pfam: PF00394; Cu-oxidase; 1.
 KW Sporulation; Complete proteome.
 FT CONFLICT 347 367 DESRKPRLASYPVQHERIO -> TRAESRSTPHLRYS
 FT FT MKDT (IN REF. 1).
 FT CONFLICT 414 420 PTRGTHP -> RHAHIL (IN REF. 1).
 FT FT GPVAVPPP -> VRCPPAA (IN REF. 1).
 SQ SEQUENCE 513 AA: 58499 MW: 836B83B458D75F87 CRC64;
 Query Match 22.4%; Score 713; DB 1; Length 513;
 Best Local Similarity 34.6%; Pred. No. 9e-45;
 Matches 183; Conservative 75; Mismatches 175; Indels 96; Gaps 18;
 Oy 66 NALPFP-----PVKQPKMTITNPVTKDIWYELKFPQORITPLPAVLGYDMSGP 121
 Db 8 DALPFPDLTKRVQO-----SKETTYEVMMECTQHLMDLPPTRLMGVNGLPFG 57
 Oy 122 PTFNVPGTFTVYRFINNA-----TVENS-----VHLHSGSPRNPFGD 159
 Db 58 PTFEVKKNENYVWLMANNLPSTHFLPIDHTIHSDSQHEPEVKTIVVHLHSGVYRPPDSOG 117
 Oy 160 WAE-----DYTFPEY---KDYTPNQAARLWYHDHAFMKTAENAFEGAGAYIIND 211
 Db 118 YPEAMFSKDEQOTPYKREYHYHPNOQRGAILWYHDHAFMKTAENAFEGAGAYIINDP 177
 Oy 212 AEDALGPSYGERDIPLLITAKYNNADGTL---RSTEGEDQD-----MGDIYHV 259
 Db 178 KERKLKLPSS--DEYDVPDLITDRINEDGSLFSPADENPSPSLNPISVPAFCGTYILV 235

OY 260 NGOPWPLNVPKRYRFRFLNAAVSRAWLLVLTSTSPNVRIPFOVIASDAGLQAPVOT 319
DB 236 NGKVPYLEPVRKRYFRVFNASMTNRYNLSDNGD-----FIQISDGLIPRSVKL 289
OY 320 SNLVAAREYEIIIDFTNAGOTLDLRNAET-NDVGEDEYATLEVMRFVSSGIVE 378
DB 290 NSFSLAPAEYDIIDFTNAGOTLDLRNAET-NDVGEDEYATLEVMRFVSSGIVE 345
OY 379 -DNSOVPSTLDVPEPPKKEPADKHFEKRSNGHY-----LINDVGADVNERLAPDE 432
DB 346 KDSERKRYLASYSVQHERIQNTKTLAQTODEYGRPVLLNNKRWHD--PYTERPK 402
OY 433 LGTVEVLELSSGSGSHPVHILVDFKILR-----TGGRGQVMPYES 476
DB 403 VGTTEIWSIINPTBG-TFPIHLVYSFRVLDLRPPDIARVQESGELSTGPAVPPSEK 461
OY 477 AGLDVWVLGEGELTTEAHQPTGTGAMHCHNLHEDNDMAVENVT 525
DB 462 -GMDTIOAHAGEVLRITAAFTGPGYSGRYVWHCHLHEDYDMRMDIT 509

RESULT 3
PHSA_STRAT STANDARD; PRT; 642 AA.
AC Q35692;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Phenoxazinone synthase (EC 1.-.-.) (PHS)..
CN PHSA.
OS Streptomyces antibioticus.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID:1890;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.
RC STRAIN-IMRU 3720;
RC MEDLINE-96011355; PubMed-7592317;
RA Hsieh C.-J., Jones G.H.;
RT Nucleotide sequence, transcriptional analysis, and glucose
RT regulation of the phenoxazinone synthase gene (phsa) from
RT Streptomyces antibioticus.;
RL J. Bacteriol. 177:5740-5747(1995).
RN [2]
RP SUBUNITS.
RX MEDLINE-82066838; PubMed-7305384;
CNOY H.A., Jones G.H.;
C "Phenoxazinone synthase from Streptomyces antibioticus: purification
C of the large and small enzyme forms.";
C Arch. Biochem. Biophys. 211:55-65(1981).
C -1- FUNCTION: CATALYZES THE LAST BUT TWO STEPS IN THE PUTATIVE
C BIOSYNTHETIC PATHWAY OF ACTINOMYCIN.
C -1- CATALYTIC ACTIVITY: 4.4-methyl-3-hydroxyanthraniloyl pentapeptide
C + 3 O(2) -> 2 actinomycinic acid + 6 H(2)O.
C -1- COFACTOR: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES WHICH
C CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE
C 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
C -1- SUBUNIT: HOMODIMER (SMALL FORM) OR HOMOHETEROMER (LARGE FORM).
C -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
C -1- SIMILARITY: CONTAINS 2 PLASTOCYANIN-LIKE DOMAINS.
C
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C between the Swiss Institute of Bioinformatics and the EMBL outstation -
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C or send an email to license@isb-sib.ch).
C
C EMBL: U04283; AAA86668.1; ALT_INIT.
C DR HSSP: P36649; 1KV7.
C DR InterPro: IPR001117; Cu-oxidase.

DR InterPro: IPR002355; MultiCu_oxidase2.
DR Pfam: PF00394; Cu-oxidase; 1.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Repeat; Metal-binding; Copper;
KW Antibiotic biosynthesis.
FT DOMAIN 86 223 PLASTOCYANIN-LIKE 1.
FT METAL 493 620 PLASTOCYANIN-LIKE 2.
FT METAL 161 161 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 163 161 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 201 201 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 203 203 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 524 524 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 527 527 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 529 529 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 602 602 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 603 603 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 604 604 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 608 608 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 613 613 COPPER (TYPE 1) (BY SIMILARITY).
SQ SEQUENCE 642 AA; 70113 MW; EDB39C0BA3364E48 CRC64;

Query Match 16.3%; Score 519; DB 1; Length 642;
Best Local Similarity 27.2%; Pred. No. 2e-30;
Matches 175; Conservative 71; Mismatches 223; Indels 174; Gaps 19;

OY 30 IEADVPEKTEVFADSLAAAGDDDESPNLYRLNLP--IPVKKPKMTINPTVTK 87
DB 11 IDPDGVADVDLADVLAKERE---QAPAGELLPFAAPLVPPVLR--ASDEVIRE 64
OY 88 DIWYEIRKPPFOORHYPTLRPATLVYDGKSPGTFVNPSTETVPERINN----- 139
DB 65 T-----ETLRFTWRRLHQLPPTLMGQIDGOVPGFTIYRQGRIRIATNRIPKSGEP 120
OY 140 -ATVE-----NSVHLGSSPSRAPDGNADVTYF 166
DB 121 VTSEVPLGPPTGPAPNTEPGRGVEPKNOVALPAMSVTLHGAGQTGGDGMADNAV 180
OY 167 PGEKKDYFFRPYQASRLMYHDHAFMKTAENAYGQAGAYIINDAEALDLSGSGEFD 226
DB 181 FGAOLSEYPDNDHATOWMYHDHANTIRMMVMAGLYGTLYVRDDEEDALGPS--GDRE 238
OY 227 IPLILFAKYNADGTLRSTEGEDDLMGDIH-----VN 260
DB 239 IPLILADRNLDTD-----EDGRNLNRLHAKYIVYQNSPENGKPIPIFPGRYTVN 290
OY 261 GQWPEFLNVPKRYRFRFLNAAVSRAWLLVLTSTSPNVRIPFOVIASDAGLQAPVOT 320
DB 291 GRIMPYADVDDGMYRLRLVNASNARIYNLVILDEDDRVPGVHQIGSDGLLRPVPEVD 350
OY 321 -NLYLAAREYEIIIDFTNAGOTLDLRNAET-NDVGEDEYATLEVMRFV 372
DB 351 FDDTLPLYSAAPARFDLVDLDFALGGRRLVDKPGAPAGTDPDGLGVRPYEMERV 410
OY 373 SSGTVEDNSQVSTL-----RDVPE-----PPHKGCP----- 399
DB 411 RETCEBESFALPEVLSSGFRMSHDIRGHLLVLTPTGTGSGGHPETMAEVEDPAD 470
OY 400 -----ADKHEKFRSNGHYLINDVGFADVNERVLARPELTVEVWELSSSG 446
DB 471 VQVPAEGVIOVTGADGRTKTYRRTAATFNDGLGFT-IGE-----GTHROMFPLNS- 520
OY 447 GMSPVHILVDFKILR-----GGGQV-----MPYESAGLKQVWL 485
DB 521 PILPHMHLADFDVLRDADVAGSFDLALGSTRPRLDPTVPPLAPNELGKDVFOV 580
OY 486 GRGETLTTEAHQPTGTGAMHCHNLHEDNDMAVENVTAME 528
DB 581 PGQGLAVMGKFDGAYGRFMVHCHLHEDNGMRRPVVMAPE 623

RESULT 4

ID	CUEO_YERPE	STANDARD:	PRT;	533 AA.
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Yersinia.			
OX	NCBI_taxid=632;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN-CO-92 / Biovar Orientalis;			
RX	MEDLINE-21470413; PubMed-11586360;			
RA	Parshall J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebathia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Katlyshev A.V., Leachter S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague."; Nature 413:523-527(2001).			
RL	-1- FUNCTION: Probably involved in periplasmic detoxification of copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake into the cytoplasm. Possesses phenoloxidase and ferrioxalase activities and might be involved in the production of polyphenolic compounds and the prevention of oxidative damage in the periplasm (By similarity).			
CC	-1- COFACTOR: This protein belongs to the multicopper oxidases which contain three distinct Cu centers known as type 1 or blue, type 2 or normal, and type 3 or coupled binuclear (By similarity).			
CC	-1- SUBUNIT: Monomer (Probable).			
CC	-1- SUBCELLULAR LOCATION: Periplasmic. It is exported via the Tat pathway (By similarity).			
CC	-1- INDUCTION: By Cu(II), at increased levels of cytoplasmic cuprous ions (Probable).			
CC	-1- DOMAIN: The methionine-rich domain could provide binding sites for exogenous copper ions. This methionine-rich region is probably important for copper tolerance in bacteria.			
CC	-1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.			
CC	-1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.			
CC	-----			
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CC	-----			
DR	EMBL; AJ14157; CAC92639.1; .			
DR	InterPro; IPR001117; Cu-oxidase.			
DR	InterPro; IPR002355; Multich_oxidse2.			
DR	Pfam; PF00394; Cu-oxidase; 1.			
DR	PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.			
KW	Oxidoreductase; Copper; Metal-binding; Periplasmic; Signal; Repeat;			
FM	Complete proteome.			
FT	SIGNAL	1	28	
FT	CHAIN	29	533	BY SIMILARITY.
FT	DOMAIN	68	164	BLUE COPPER OXIDASE CUEO.
FT	DOMAIN	165	425	PLASTOCYANIN-LIKE 1.
FT	DOMAIN	426	533	PLASTOCYANIN-LIKE 2.
FT	DOMAIN	356	415	PLASTOCYANIN-LIKE 3.
FT	METAL	102	102	MET-RICH.
FT	METAL	104	104	COPPER (TYPE 2) (BY SIMILARITY).
FT	METAL	142	142	COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL	144	144	COPPER (TYPE 3) (BY SIMILARITY).
FT	METAL	458	458	COPPER (TYPE 1) (BY SIMILARITY).
FT	METAL	461	461	COPPER (TYPE 2) (BY SIMILARITY).
FT	METAL	463	463	COPPER (TYPE 3) (BY SIMILARITY).

Query Match	12.7%	Score 405.5	DB 1	Length 533
Best Local Similarity	27.1%	Pred. No. 3.2e-22		
Matches 146	Conservative 57	Mismatches 217	Indels 119	Gaps 18
FT METAL	514	514	COPPER (TYPE 3) (BY SIMILARITY).	
FT METAL	515	515	COPPER (TYPE 1) (BY SIMILARITY).	
FT METAL	516	516	COPPER (TYPE 3) (BY SIMILARITY).	
FT METAL	520	520	COPPER (TYPE 1) (BY SIMILARITY).	
FT METAL	525	525	COPPER (TYPE 1) (BY SIMILARITY).	
SQ SEQUENCE	533 AA	58328 MW	ED1570C9E9B1C135 CRC64	
Query Match	12.7%	Score 405.5	DB 1	Length 533
Best Local Similarity	27.1%	Pred. No. 3.2e-22		
Matches 146	Conservative 57	Mismatches 217	Indels 119	Gaps 18
OY	68	LPIDPPVOPK---MTNPNVTKGDVWYEEIEKPFQGRITVPLRLRATLV---	GYDGMSPG 121	
DB	34	LPIDPILDPDANGKINLNIQTGSVWL-----PSTNIQTWGVYGNLLG	76	
OY	122	PTFNVPRTETVFVRFINNAIVENSYHLHSGPSRAEFDGMADVTFFPGEYKDYFPNPYOSA	181	
DB	77	PAIRLQGRKAVTIDITNLPRATVYHMHGLEIPGEVDGPPALDOPGAKRQVFAVEQPA	136	
OY	182	RLWYTHDIAFMKTAENAFVGOAGATYINDEADALGLPSGGEFDPILRLTAKYNNAGOT	241	
DB	137	ATCFWFHPHTHSGHGVAMGLGGLVLLIDDSOSETPLRLPKONGCVDDIPVILDDKLDDKHQ	196	
OY	242	LRSTGEEDOD-----WGDVYHVGOPMPFLNVPORRY-RPRFLNAAVSRAMLVYL	291	
DB	197	V-----DYOLDVMTAAVGFGRDLRLTNGVYR-QQILPRGMVRLRLNGCARSLNAL	249	
OY	292	VRTSSPNVRIPEOVIASDAGILQAEVQTSNLYLAVAREYETIIDFTNAGOTLDRNVAE	351	
DB	250	-----SPGRPMYVIASDGLILAEVYVRELPILMGEFEVLVDTRD--GQSLDLVTLPV	301	
OY	352	TNDVDEDEYARTLEVMAFVYVSSGVEEDNSQV-PSLTDVPPRPRIKGRADKHF-----	404	
DB	302	TOMGTALAPFQPLPELRIQPS---LALGSOVLPELSLVILDELADVTGVQERFQLMMDP	358	
OY	405	KFERSNGHYLI-----NDVGRFAD-----	422	
DB	359	KLDIMGKALVARYGKMRKMAAGMNNHGMGMDHGNRDMDSOGKKMGDHTGMNAPAFN	418	
OY	423	-----VNERVLAKPE-----LGTVEWELENSSGSHPVHHLVDLFKLKRTGGRGQ	470	
DB	419	FSHNRIRIGKAFKAFMTPEAFDAKQGYEKWTISGEGDMALHPFHVHGTQFRILTENG----	474	
OY	471	VMPPE-SAGLGDVYWL--GREETLIEAHQYPMWGAVMYHCHNLHENDMMAYVNPNTA	526	
DB	475	KPPEHHRGRMGDIVRVEGARSEILVRFNLYLAPSTPYMAHCHLLEHEDTGMGLGTVA	533	
RESULT 5				
CUEO_SALTI				
ID_CUEO_SALTI	STANDARD	PRT	536 AA	
AC	0829E1			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Blue copper oxidase cueo precursor (Copper efflux oxidase).			
GN	CUEO OR STY0190.			
OS	Salmonella typhi.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Salmonella.			
OX	NCBI_TaxID=601;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CT18;			
RX	MEDLINE=21534947; PubMed=11677608;			
RA	Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,			
RA	Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahin M.,			
RA	Baker S., Basham D., Brooks K., Chillingworth T., Conerton P.,			
RA	Crocin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,			
RA	Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jajels K.,			
RA	Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,			
RA	Quail M., Rutherford B.G., Simmonds M., Skelton J., Stevens K.,			
RA	Whitehead S., Barrrell B.G.;			

RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 RT *enterica* serovar Typhi C718.";
 RL Nature 413:848-852(2001).
 CC -1- FUNCTION: Probably involved in periplasmic detoxification of
 CC copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake
 CC into the cytoplasm. Possesses phenoloxidase and ferroxidase
 CC activities and might be involved in the production of polyphenolic
 CC compounds and the prevention of oxidative damage in the periplasm
 CC (By similarity).
 CC -1- COFACTOR: This protein belongs to the multicopper oxidases which
 CC contain three distinct Cu centers known as type 1 or blue, type 2
 CC or normal, and type 3 or coupled binuclear (By similarity).
 CC -1- SUBUNIT: Monomer (probable).
 CC -1- SUBCELLULAR LOCATION: Periplasmic. It is exported via the Tat
 CC pathway (By similarity).
 CC -1- INDUCTION: By Cu²⁺, at increased levels of cytoplasmic cuprous
 CC ions (Probable).
 CC -1- DOMAIN: The methionine-rich domain could provide binding sites for
 CC exogenous copper ions. This methionine-rich region is probably
 CC important for copper tolerance in bacteria.
 CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
 CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: AL627265; CAD01326.1;
 DR Interpro: IPR001117; Cu-oxidase.
 DR Interpro: IPR002355; Multicopper oxidase.
 DR Pfam: PF00394; Cu-oxidase; 1.
 DR PROSITE: PS00080; MULTICOPPER-OXIDASE2; 1.
 DR OXIDOREDUCTASE: Copper; Metal-binding; Periplasmic; Signal; Repeat;
 KW Complete proteome.
 FT SIGNAL 1 28
 FT CHAIN 29 536 BY SIMILARITY.
 FT DOMAIN 67 163 BLUE COPPER OXIDASE CUEO.
 FT DOMAIN 164 430 PLASTOCYANIN-LIKE 1.
 FT DOMAIN 431 536 PLASTOCYANIN-LIKE 2.
 FT DOMAIN 355 420 PLASTOCYANIN-LIKE 3.
 FT METAL 101 101 MET-RICH.
 FT METAL 103 103 COPPER (TYPE 2) (BY SIMILARITY).
 FT METAL 103 103 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 141 141 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 143 143 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 463 463 COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL 466 466 COPPER (TYPE 2) (BY SIMILARITY).
 FT METAL 466 466 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 519 519 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 520 520 COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL 521 521 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 525 525 COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL 530 530 COPPER (TYPE 1) (BY SIMILARITY).
 SQ SEQUENCE 536 AA; 58624 MW; 2410581D287C3BE0 CRC64;

Query Match 12.38; Score 391; DB 1; Length 536;
 Best Local Similarity 25.88; Pred. No. 3,7e-21;
 Matches 140; Conservative 68; Mismatches 215; Indels 120; Gaps 18;

QY 65 RNALPIPVKQPMITNPYTGKDIWYELIKRPFQORITPLRALVGYDQMSPTPT 124
 DB 31 RPLALPDP-----LPLADASNR---MQLIVRAGOSTF--AGKNATWTWYNGNLGPAY 78
 QY 125 NVPRTGETVVRFINNATVENSVALHGSPPSRAPFGMAEDVTFPGEXYKDYFPYVQSARL 184
 DB 79 QLHKGSVYVDIHNOALAEPTLHMHGELFPGYDGGQGITRAGGRTVTFTRQQRATC 138
 QY 185 WYIDAFAMKTAENAVYGOAGAVYIINDAEDALGPSYGEFDIPLITAKYVYADGTLRS 244
 DB 139 WHPHRRKGTGROVAVMAGLVLIEDDELIRKRLRPQWGIQDVVPIIDKRFSADGQI-- 196

QY 245 TEGEDQDL-----MGDYIHVNGQWPFLLNQPRKRRPFLNAAVSRAMLLYVTS 295
 DB 197 ----DYQDITPAVAGFEGDYLNLNGAIYPOHSAPKGMRLRLNGCNARS-----LNTIA 248
 QY 296 SPNVRIPROVIASDAGLLOAVQVTSNLTAAVEREYIITDFNAGQTLDRNVAETNDV 355
 DB 249 SDN---RPLVIASDGLLAEPVKTELPLMGEREVLVDSD--GRKFDLVTI-PSVQM 303
 QY 356 G-----DEDEYARTLEVMRFVYSSGVEDNSQVPSITRDVPFPPEKGRADKHKF--- 406
 DB 304 GMAIAPFDPKPRPVNRIOPLR-ITASGT-----LPDITFTPALPSLGLTVRNLIKLSMD 356
 QY 407 -----ERNGHYLLINDVFAPD----- 422
 DB 357 PRLDMGQMLAKTKYGAQAMSGMDHDSNNHMGAGNMGHGEMDGNMDHSGMNHGAMGM 416
 QY 423 -----VNERV--LAKP-----ELCTVEWELENSGSGSPHVIHLVDFILK 463
 DB 417 NHGKRFDPHNANFINGOVFDKNNKPMFAQKQHRHERVYISGVDMILHFPFHIGQFRILS 476
 QY 464 RTGGRGOVMPYESAGLKDQVWL--GRGETLTIEAHYQPTGAYVMHCHNLIHEDNDMAV 521
 DB 477 E--NGKAPAAHRTGMKDTVYVEGGISEVLVKFDHDAPEKHAAYMAHCHLLEHPTGMMLG 533
 QY 522 FNV 524
 DB 534 FTV 536

RESULT 6
 CUEO_SALTY STANDARD; PRT; 536 AA.
 AC Q8ZRS2; Q938E6;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Blue copper oxidase CUEO precursor (Copper efflux oxidase).
 GN CUEO OR CUID OR STM0168.
 OS *Salmonella typhimurium*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Salmonella*.
 OX NCBI_Taxid=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee I.S., Lim S.Y., Choi S.-Y.;
 RT "cuid", a gene encoding a multicopper oxidase from *S. typhimurium*:
 RT cloning and characterization.";
 RN submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., All J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 CC -1- FUNCTION: Probably involved in periplasmic detoxification of
 CC copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake
 CC into the cytoplasm. Possesses phenoloxidase and ferroxidase
 CC activities and might be involved in the production of polyphenolic
 CC compounds and the prevention of oxidative damage in the periplasm
 CC (By similarity).
 CC -1- COFACTOR: This protein belongs to the multicopper oxidases which
 CC contain three distinct Cu centers known as type 1 or blue, type 2
 CC or normal, and type 3 or coupled binuclear (By similarity).
 CC -1- SUBUNIT: Monomer (probable).
 CC -1- SUBCELLULAR LOCATION: Periplasmic. It is exported via the Tat
 CC pathway (By similarity).

CC -1- INDUCTION: By cuer, at increased levels of cytoplasmic cuprous
 CC ions (probable).
 CC -1- DOMAIN: The methionine-rich domain could provide binding sites for
 CC exogenous copper ions. This methionine-rich region is probably
 CC important for copper tolerance in bacteria.
 CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
 CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AY053397; AAL15149.1; -
 DR EMBL: AE008702; AAL19132.1; -
 CC Skysene: SG77777; cuco.
 CC InterPro: IPR001117; Cu-oxidase.
 CC Pfam: PF00394; Cu-oxidase; 1.
 CC PROSITE: PS00080; MULTICOPPER OXIDASE2; 1.
 DR Oxidoreductase; Copper; Metal-binding; Periplasmic; Signal; Repeat;
 KM Complete proteome.
 FT SIGNAL 1 28 BY SIMILARITY.
 FT CHAIN 29 536 BLUE COPPER OXIDASE CUO.
 FT DOMAIN 67 163 PLASTOCYANIN-LIKE 1.
 FT DOMAIN 164 430 PLASTOCYANIN-LIKE 2.
 FT DOMAIN 431 536 PLASTOCYANIN-LIKE 3.
 FT DOMAIN 355 420 MET-RICH.
 FT METAL 101 101 COPPER (TYPE 2) (BY SIMILARITY).
 FT METAL 103 103 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 141 141 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 143 143 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 463 463 COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL 466 466 COPPER (TYPE 2) (BY SIMILARITY).
 FT METAL 468 468 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 519 519 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 520 520 COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL 521 521 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 525 525 COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL 530 530 COPPER (TYPE 1) (BY SIMILARITY).
 FT CONFLICT 322 323 LR -> F (IN REF. 1).
 FT CONFLICT 334 334 L -> F (IN REF. 1).
 FT SEQUENCE 536 AA; 58625 MW; E4C04555AF621DF CRC64;
 SQ
 Query Match 12.2%; Score 390; DB 1; Length 536;
 Best local similarity 25.8%; Pred. No. 4,4e-21;
 Matches 140; Conservative 68; Mismatches 215; Indels 120; Gaps 18;
 Oy 65 RNALPPIPVKOPKMTITNPVTGKDIWYEIEIKPPQRIYPLTRATLVGYDGMSPGPTF 124
 Db 31 RALPIPIP-----LITADASNR-----MOLYKAGQSF--AGKNAITWGVGNLGRVAV 78
 Oy 125 NVPRGTEVTVRFINNATVENSVHLHSGSPRAPFDGMAEDVTFPGYKDYFPNYSARLL 184
 Db 79 QLHGKSVTVYDINHDLADDTLHMGLEIPGIVDGGPGLIIPAGSTRVTFPEQRAATFC 138
 Oy 185 WYHDAEFKTAENAFVFGAGAVIINDEADALGLPSGGEFPIPLILAKTYNADGTLRS 244
 Db 139 WHPHKGKTRQVAMGLAGLVLEDDIRKRLPKWGGIDVPIIDDKRSADGQI-- 196
 Oy 245 TEGEDODL-----MGDYIHNVGQMPFLNVPQRYRFRFLAAVSRAWLTVRTS 295
 Db 197 -----DYQIDMTAAVNGFGDTLLTNGALTYPOHSAPKGLRLKLGNCARF-----LNTAA 248
 Oy 296 SPNVRIPQVIASAGALLQAPVQSNLYLAAREYIIITDFNAGQTLDLNNVATNDV 355
 Db 249 SDN--RPLYLVIASDGLLAEPVKTELPLNGEREVLVDISD--GKAFDLTVL--PVSQM 303
 Oy 356 G-----DEDEYARLEVMRFRVSSGIVEDNSQVPSITLDVPPPHKSGPADKHEKF--- 406

Db 304 GNAIAPFDKPHPMRIQPLR-ITASGT-----LPDLITMPALPSLEGLTVRNLIKLSMD 356
 Oy 407 -----ERSNGHYLINDVGPAD----- 422
 Db 357 PRLDMGQMMLKRYGAQAMSGMDHSMNAHOGGNGHGEHDHGMDSGNHAGMGM 416
 Oy 423 -----VNERV--LAKP-----ELGTVWELENSSGWSHPVHLVDPKILK 463
 Db 417 NHGKFDFFNANFINGQVFDNMRPFAOKGRHERWVLSGVDMLHPFHIGTOFRILS 476
 Oy 464 RKGSGQVWPYPSASLAKDYVNL--GRGETLTLEATYQFTGAYMHCHNLHEDDMAY 521
 Db 477 E---NGKAPAAHRTGMKDTVRVEGISEVLKFDHDAKREHAYMAHCHLLEHEDGMMLG 533
 Oy 522 FNV 524
 Db 534 FTV 536
 RESULT 7
 CUEO_ECOLI
 ID CUEO_ECOLI STANDARD; PRI; 516 AA.
 AC P36649; P75655;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Blue copper oxidase cuco precursor (Copper efflux oxidase).
 GN CUEO OR B0123.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / M3110;
 MEDLINE=94261430; PubMed=8202364;
 RX Fujita N., Mori H., Yura T., Ishihama A.;
 RT "Systematic sequencing of the Escherichia coli genome: analysis of
 RL the 2.4-4.1 min (110,917-193,643 bp) region."; Nucleic Acids Res. 22:1637-1639(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
 [3]
 RP SEQUENCE OF 29G2.
 RC STRAIN=K12 / EMG2;
 MEDLINE=97443975; PubMed=9298646;
 RX Link A.J., Rodison K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 RL in the genome of Escherichia coli K-12."; Electrophoresis 18:1259-1313(1997).
 [4]
 RP IDENTIFICATION BY MASS SPECTROMETRY.
 RC MEDLINE=99420866; PubMed=10493123;
 RX Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
 RT "Enrichment of low abundance proteins of Escherichia coli by
 RL hydroxyapatite chromatography."; Electrophoresis 20:2181-2195(1999).
 [5]
 RP POSSIBLE FUNCTION IN COPPER HOMEOSTASIS.
 RC MEDLINE=21125583; PubMed=11222619;
 RX Grass G., Rensing C.;
 RT "Genes involved in copper homeostasis in Escherichia coli."; J. Bacteriol. 183:2145-2147(2001).
 [6]
 RP POSSIBLE FUNCTION IN COPPER HOMEOSTASIS.

Db 513 GFTV 516

RESULT 8
CUBO_ECO57 STANDARD; PRT; 516 AA.
AC Q8X947;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Blue copper oxidase CUBO precursor (copper efflux oxidase).
GN CUBO OR 20133 OR ECS0127.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN (1)
SEQUENCE FROM N.A.
STRAIN-O157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grobcek E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533(2001).
RN (2)
SEQUENCE FROM N.A.
STRAIN-O157:H7 / RIMD 0509952;
RC MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kihara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12";
RL DNA Res. 8:11-22(2001).
CC -1- FUNCTION: Probably involved in periplasmic detoxification of copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake into the cytoplasm. Possesses phenoloxidase and ferroxidase activities and might be involved in the production of polyphenolic compounds and the prevention of oxidative damage in the periplasm (By similarity).
CC -1- COFACTOR: This protein belongs to the multicopper oxidases which contain three distinct Cu centers known as type 1 or blue, type 2 or normal, and type 3 or coupled binuclear (By similarity).
CC -1- SUBUNIT: Monomer (Probable).
CC -1- SUBCELLULAR LOCATION: Periplasmic. It is exported via the Tat pathway (By similarity).
CC -1- INDUCTION: By Cu²⁺, at increased levels of cytoplasmic cuprous ions (Probable).
CC -1- DOMAIN: The methionine-rich domain could provide binding sites for exogenous copper ions. This methionine-rich region is probably important for copper tolerance in bacteria.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
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CC
CC EMBL; AEO05188; BAG54427.1; -
CC EMBL; AP002550; BAB33550.1; -
CC InterPro: IPR001117; Cu-oxidase.
CC InterPro: IPR002355; Multicopper oxidase2.
CC Pfam; PF00394; Cu-oxidase; 1.

DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Copper; Metal-binding; Periplasmic; Signal; Repeat;
KW Complete proteome.
FT SIGNAL 1 28 BY SIMILARITY.
FT CHAIN 29 516 BLUE COPPER OXIDASE CUBO.
FT DOMAIN 67 163 PLASTOCYANIN-LIKE 1.
FT DOMAIN 164 410 PLASTOCYANIN-LIKE 2.
FT DOMAIN 411 516 PLASTOCYANIN-LIKE 3.
FT DOMAIN 355 400 MET-RICH.
FT METAL 101 101 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 103 103 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 141 141 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 143 143 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 443 443 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 446 446 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 448 448 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 499 499 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 500 500 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 501 501 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 505 505 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 510 510 COPPER (TYPE 1) (BY SIMILARITY).
SQ SEQUENCE 516 AA; 56702 MW; 7AD387C79780386 CRC64;
Query Match 12.1%; Score 385.5; DB 1; Length 516;
Best local similarity 25.9%; Pred. No. 8.8e-21;
Matches 141; Conservative 66; Mismatches 208; Indels 129; Gaps 19;
OY 66 NALPL-----PPYKPKMTITNVYCKDITWYEIEIKPPQQRITPL----- 107
DB 17 SALPLMSRAVFAERPLIPDLITLTD-----RNRIQLITGAGQSTFG 60
OY 108 -RPATIVGYDGMSPGFENVPRTETVRFENNAFTVENSVALHGSPSRAPFGWAEDVTF 166
DB 61 EKTATWYQYNNLGLPAKLRGKAVYDIYNOLTEETLTHMGLVNGEVDGPGQGITP 120
OY 167 PGEYKDYFFPYQASARLLMYHDAFMKTAENAYFGQAGAYIINDAEDALGPGCYGEED 226
DB 121 PGKRSVTLVNDQPAATCFMHPHOGKTRGQVAMGLAVIYEDDELTKMLPKWGIID 180
OY 227 IPLLITAKYVADGTLSTBEEDDL-----KGVHVNQMPFLVQPRKY-RF 276
DB 181 VPIVVDKFFSADQI-----DYQLDMTAAGVFGDTLLTNATYP-QHAARGWLRL 233
OY 277 RFLNAASRAMLLLVRTSSPNVRLIPQVIAADGLQAPQTSNLYLAVEREITIDF 336
DB 234 RLNGCNAKS-----LNRATSDN--RPLVIAISDGLLPEPKVVELPLMKERREVLVEV 287
OY 337 TN---FAGQTLDRNVAETNDVGDDEYARTLEVRRVSSGTVEDNSQVSTLDVFP 393
DB 288 NDNKPFPLVTLPLVPSQMGWA--IAPFDKPPHVPMRIQPIAISA-----SGALPDLTSSPAL 340
OY 394 PKRGPA-----DKH----- 403
DB 341 PSLGLTVRKQLQSLMDPMLDMGMQMLMEKGGDAVNGMDHSQMGHNGNNHMHNG 400
OY 404 -FKERSNGHYLINDVGFADYNERVLAKEPLGTVEVELESSGSGSPHYIHLVDKIL 462
DB 401 KFDHHNAN---KINGQAF-DNKKRMPAAK-GQYERNVVISGVMGLMHPFIHOTOIRIL 455
OY 463 KRTGRCQVMPYESAGLKVYVL--GGETITTEAHYQWPTGAYMHCNIIHEDDMA 520
DB 456 SE---NCKPRAHRAQWMDTFKVGNSVYLKFNHDAKPERAYAMACHLLEHEDTGML 512
OY 521 VENV 524
DB 513 GFTV 516

RESULT 9
SUFL_ECOLI STANDARD; PRT; 470 AA.
AC P26648;
DT 01-AUG-1992 (Rel. 23, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein sufi precursor.
 GN SUFI OR B3017.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 NC NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX BLATNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
 RILEY M., COLLADO-VIDES J., GLASNER J.D., RODE C.K., MAYHEW G.F.,
 GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
 MAU B., SHAO Y.,
 RA "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 [2]
 RN [2]
 RP SEQUENCE OF 1-89 FROM N.A.
 RC MEDLINE=92212294; PubMed=1557036;
 RX COLEMAN J.;
 RA "Characterization of the Escherichia coli gene for
 1-acyl-sn-glycerol-3-phosphate acyltransferase (Plsc).";
 RL Mol. Gen. Genet. 232:295-303(1992).
 [3]
 RN [3]
 RP SEQUENCE OF 28-39.
 RC STRAIN-K12 / EMG2;
 RX MEDLINE=97443975; PubMed=9298646;
 RA LINK A.J., ROBISON K., CHURCH G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 in the genome of Escherichia coli K-12.";
 RL Electrophoresis 18:1259-1313(1997)
 CC -1- FUNCTION: INVOLVED IN CELL DIVISION, SUPPRESSES A FIRST MUTATION.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
 CC
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 DR EMBL: U28377; AAA69185.1; -;
 DR EMBL: AE000384; AAC76053.1; -;
 DR EMBL: M63491; AAA24398.1; -;
 DR PIR: S20461; S20461.
 DR HSSP: P36649; 1KV7.
 DR Ecogene: EG11376; sufi.
 DR InterPro: IPR001117; Cu-oxidase.
 DR Pfam: PF00394; Cu-oxidase; 1.
 DR Periplasmic; Signal; Complete proteome.
 DR KW SIGNAL 1 27
 DR FT CHAIN 28 470 PROTEIN SUFI.
 DR FT DOMAIN 68 164 PLASTOCYANIN-LIKE.
 DR SO SEQUENCE 470 AA; 51858 MW; C643A5ACB146688 CRC64;
 Query Match 10.7%; Score 340.5; DB 1; Length 470;
 Best Local Similarity 26.9%; Pred. No. 1.5e-17;
 Matches 139; Conservative 62; Mismatches 176; Indels 139; Gaps 20;
 QY 20 GIMDGSHEIENAVDEVKTEVRADSLAAGDDWESPYNLLIRALFLIPYKPKMT 79
 DB 13 GAGCAGAVPLK-----SAAG-----OQPLVPLLESR-- 43
 QY 80 ITNPVYKDIWYEIEIKPROGRITPLRP---ATLVGYDGMSPGFENVPGRGTVYRF 136
 DB 44 -----RGQPLFM-----TVQRAHMSFTGTASVWGINGRILGLPTIRWKGDDVKLYI 91
 QY 137 INNATYENSV-----HLHGSFSR--APFDGMAEDVTPEYKDYPPNYQSARILW 185

DB 92 SNRLTENVSMTVAGIQAQVPCGLMGCPARMMSPNADMAP-----VLPIRONATLW 140
 QY 186 YHDAEFKTKTAEENAFGAGAYITNDEADNAGLPSGGERDIPILITAKYNNADGTRST 245
 DB 141 YHANTPRTAQOQYVINGNAGMWLVEVSKSLPIPNHGVDFPVIIDKRLDNFGPEYN 200
 QY 246 EGEDQDLMGVIVHNGQPMPEFLNVQPKRYRFRPRAVSAVRAMLLYLVRTSSPNVRIPOV 305
 DB 201 EPGSGGVGDTLVNNGVQSPVVEVSRGVRLRLNANSNRVQGM-----NDGRPLHV 254
 QY 306 IASDAGLLQAPVQTSNLYLAVEREITIDFTNAGOTDLRLNVAETNDVGE-----DE 360
 DB 255 ISGQGLPAPVSVKQSLALPGERREILVMSN-----GDEVSTIRGE 297
 QY 361 YARLEVMRRVSSGTYEDNSQVPSLT-----RDVPPPKKEPAD 401
 DB 298 AASTVDRIK-----GFEPSSTLVSTVLTPRTGLPLVTSDLPMLLPETIMAGSPI- 351
 QY 402 KHFEKRSNGHYLLINDGFA---DVNERVLAKEPDELGVWELENSSGGSHPVHLY 457
 DB 352 -----KSRDISLDDPGINGQMLDVN-RIDVTAQOGTWERMYRADE---PQAFHIEGV 401
 QY 458 DFKILKRTGRGQVMPY-ESAGLKDVYL-GRGETL 491
 DB 402 MFOIRNVNG-----AMPPEDRGMKDTVMVDGQVELL 433
 RESULT 10
 SUFI_SALTY STANDARD; PRT; 470 AA.
 AC P40799;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein sufi precursor.
 GN SUFI OR STM3172 OR STY3349.
 OS Salmonella typhimurium, and
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 NC NCBI_TaxID=602, 601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES-S.typhimurium; STRAIN-LT2;
 RA Cong J., Schmid M.B.;
 RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
 [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McCelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 Courtney L., Portwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 Leonard S., Nguyen C., Scott K., Holmes A., Grewel N., Mulvaney E.,
 Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
 Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 LT2.";
 RL Nature 413:852-856(2001).
 [3]
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES-S.typhi; STRAIN-CF18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 Krogue A., Larsen T.S., Leather S., Moule S., O'Goira P., Parry C.,
 Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 Whitehead S., Barrall B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 enterica serovar Typhi CF18.";
 RL Nature 413:848-852(2001).

Search completed: July 1, 2003, 10:39:24
Job time : 27 secs

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CC -1- FUNCTION: INVOLVED IN CELL DIVISION, SUPPRESSES A FTSI MUTATION
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).
CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to a
CC frameshift in position 413.
CC -----
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CC -----
CC DR EMBL: U09309; AAA56679.1; ALT_FRAME.
CC DR EMBL: AE008845; AA122046.1; -.
CC DR EMBL: AL627277; CAD03004.1; -.
CC DR HSSP: P36649; IKV7.
CC StyGene; SG10522; sufi.
CC InterPro: IPR001117; Cu-oxidase.
CC Pfam: PF00394; Cu-oxidase; 1.
CC Periplasmic; Signal; Complete proteome.
CC FT SIGNAL 1 27 FT SIMILARITY.
CC CHAIN 28 470 PROTEIN SUFI.
CC DOMAIN 68 164 PLASTOCYANIN-LIKE.
CC SEQUENCE 470 AA; 51858 MW; 61B84D4D2B025FB CRC64;

Query Match 10.1%; Score 323.5; DB 1; Length 470;
Best Local Similarity 25.8%; Pred. No. 2.7e-16;
Matches 142; Conservative 58; Mismatches 190; Indels 161; Gaps 21;

QY 1 MLFSWQLAASGLSGVIGIPMDGSHPIEAVDEVEKTEVFADSLAAAGDDWESPPY 60
DB 1 MSFSRQFLQAS-----GIALCGAIPLR-----NAAGQ----- 30
QY 61 NLLRYNALPIPPVKOPKMITINPYTGKDIWYIEIKPPQORIPYTLR-----PA 110
DB 31 ----QQLPVPPLLESRR-----GQPLEMTLQRAHWSFYQGTTRA 65
QY 111 TLVGYDGMSPGTFVPRGTETVYVFINNATYENSV-----HLGSPSR--APFDG 159
DB 66 FPMGNGRYRIGTPIRWKGGDVKLIYSNRLAENVSMYVAGLIVPGPLMGGPARMSPNAD 125
QY 160 WAEDVTFPEYKDYFPNYQSAKRLMYHDHAFMKTAENAYFGQAGAYIINDAEDALGIP 219
DB 126 WAP-----VLPIRQSAATLWYHANTPNRTAQYNGLAGMMLVEDDISKTLP 174
QY 220 SGYGEFDIPLILTAKYNAADGTLNSTEGEDODLMDGVTHVNGQPMPEFLNVOPKTYRFRFL 279
DB 175 NHYGVDDEPVIIDKRLDNFGTPEXSEPGSGGVGDFTLLVNGAQSPYVEVSRGWRLRL 234
QY 280 NAAVSRAVLTLVTRSSPNVRIPFQVYASDAGLLQAPQTSNLYLAVEREILIDTFNF 339
DB 235 NANSRRYQLOMSDGRA-----LHVISGDQGFELPAVSVKOLSLAPGERREILVDMTN- 287
QY 340 AGQTLDLRNVAETNDVDE-----DEVARTLEVRFVSSGTVEDNSQVPSYL----- 387
DB 288 -----GDEVSLTGCGLAASIVDIR-----GFEPPSSILVSTLYLTLPRT 326
QY 388 -----RDVFPFPHKEGPAKHFKEFSNGHYLLINDVGA---DYNERVLAKP 431
DB 327 GLPLPLVTNLPMLRLPTEIMSGAPV-----RSRDISLGDDPGINGQLMDVN-RIDITA 378
QY 432 ELGTYVEWLENSGCGMHPVHIHLYDFKILKRTGSGQVMPY-ESAGIKDVMVLGRGET 490
DB 379 QOGTWERVTVR---ADMPQSFHIEGVSFILRVNG---AMFEPEDRGMKDTVMVD-GQV 430
QY 491 LTIHAHYOP-W 500
DB 431 ELLVYYGQPSW 441
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	RESULT	1
Q9P8C3	ID	PRELIMINARY; PRT; 602 AA.
DY	Q9P8C3	
DT	01-OCT-2000 (TrEMBLrel. 15, Created)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)	
DE	Polyphenol oxidase precursor.	
CN	PROB.	
OS	Acronium murorum.	
OC	Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	
OC	Hypocreales; Hypocreaceae; mitosporic Hypocreaceae; Acronium.	
OX	NBI_TaxID=45278;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=CBS 157.72;	
RX	MEDLINE=21268855; PubMed=11375170;	
RA	Goka R.J., van der Heiden M., Swarthoff T., Verrips C.T.;	
RT	"Cloning of a phenol oxidase gene from acronium murorum and its expression in Aspergillus awamori."	
RL	APPL. ENVIRON. MICROBIOL. 67:2610-2616(2001).	
DR	EMBL: A0711104; CAB75422.1; -	
DR	InterPro: IPR001117; Cu-oxidase.	
KW	Pfam: PF00394; Cu-oxidase; 1.	
FT	SIGNAL.	
FT	CHAIN 1 21 POTENTIAL.	
FT	CHAIN 62 602 POLYPHENOL OXIDASE.	
SQ	SEQUENCE 602 AA; 66920 MW; 0303D991405228A3 CRC64;	
	Query Match 53.5%; Score 1705; DB 3; Length 602;	
	Best Local Similarity 60.6%; Pred No.14e-122;	
	Matches 325; Conservative 72; Mismatches 125; Indels 10; Gaps 4	
QY	57 SEPNLLLYRNALPIPEVKKPKMILITNPYTGKDIWYEIEIKRFOORITPTLRPATLVGYD 116	
	::: ::: ::: ::: ::: ::: ::: :::	
DY	65 SAYVT-LFQAPLSIPGVKEPLEFTYNPNNGSIDIYEIEIKHFSQVFPDLGPAIDLGYD 123	
	: ::: : ::: ::: ::: ::: ::: :::	
QY	117 GMSPGCTEENPVGTETVVAFINNAIVENSVAHLHGSPSAPPDGAEDVTFPGEEKDYFF 176	
	: ::: : ::: ::: ::: ::: ::: :::	

DB 124 GISPPTFIQEGRSVVRFNKATVESSIHLSGFSRAWDMAEDVTNPGEYDYYP 183
QY 177 NYOSARLLMYHDHAFMKTAENAYFGACAGYIINDAEDALGSPSGEGEDILITAKKY 236
DB 184 NAQAQRFWSYHDHAFMKTAENAYFGACAGYIINDAEDALGSPSGEGEDILITAKKY 243
QY 237 NADGRLSTEGEDOLMGDVIHNGCPMPEFLAVQPRKTRERFLNAAVSRAMLLYLVRSS 296
DB 244 NSDGLTFSTGKTOILMGDVIQVNGVPMPEYEPVEPRKFRLLDAVSRFSFLYEVDFAD 303
QY 297 PVVRFPVOIASDGLAPVQTSNLYLAVEREYIIDFTNPAQOTDLRVAENNDG 356
DB 304 EDTRFPVOIASDGLLEPPTYSKLVLSIAERTIILDSOEGKTIELRNEPVGGLG 363
QY 357 DEDEVARTLEVRFFVSSGTYE--DNSQVSTLRDVPPEPRKHEKFEKERSNGHYL 414
DB 364 IEVNDTDTDKVRFVNAAGPLSSPDTSVPSSTLRDVPSPSSSTIIDSFRARAFAGQMS 423
QY 415 INDVGFADYNEVYLAKEPELGYEVELENSGSGSHPVHILVDRKILKRTG-----R 468
DB 424 INGTFSDVENLLANVPLGTVOQLTNAAQGMTHPIHILVDFKILSRGAATGATTR 483
QY 469 GQVMPYESAGLKDVYVLMGRGETLTLEAHYQPTGAYMTHCHNLHEDNDMAVFNVTAME 528
DB 484 G-VEPYESAGLKDVYVLMGRGETLTLEAHYQPTGAYMTHCHNLHEDNDMAVFNVTAME 542
QY 529 EKGYLEDEDEPMNKRMAVRYNRDFFHARAGNFAESTITARQELADEQEPYRLD 584
DB 543 DYGYNSTALADPMQDEFRAPKPYDNDVEYRENAFSTDEIAEQVQMASTLYPDPND 598

RESULT 2

QY 093M03 PRELIMINARY: PRT: 475 AA.
AC 093M03;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Oxidoreductase-like protein.
GN AUR21.
OS Streptomyces aureofaciens.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1884;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=CM3239;
RC Kormanec J., Bistakova J., Novakova R., Homeroza D., Rezuchova B.,
"Cloning and characterization of a new polyketide gene cluster in
Streptomyces aureofaciens CM3239,"
Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
EMBL: AY033994; AAK61713.1;
SEQUENCE 475 AA; 52602 MW; A2ED9A4C38DD0C9 CRC64;

Query Match 19.2%; Score 612.5; DB 2; Length 475;
Best Local Similarity 34.3%; Pred. No. 1.1e-38;
Matches 174; Conservative 66; Mismatches 196; Indels 71; Gaps 21;
QY 39 TEVFADSLAAGDDMESPPYNLRYNALPIPVYKOKMITNVTGKDIWYIEIKR 98
DB 21 SQVAASSLATA-----EAPRI-VFPAHAMPKTKLP-----TSTTATSDL--YEIRMQE 67
QY 99 FQQRITPLRATLVGDMSPGPTFNVPRGTEVVRFINNATVENSVLHSGSPRAPFD 158
DB 68 AOVEIVKGLM-SKVTYDGTFFPPTIRATQGREVVYVQINELQVNTAVHLGAHLSHD 126
QY 159 GMADVTFPGEYKQIYFPNYOSARLLMYHDHAFMKTAENAYFGACAGYIINDAEDALGL 218
DB 127 GLPMDTIVPGEERYRYRPNQPAASLWYHDHAFMKTAENAYFGACAGYIINDAEDALGL 186
QY 219 PSQGEEDIPILITAKKYNADGTLRSTEGEDOLMGDVIH--VNGQPMPEFLNVPKRYRF 276
DB 187 PS--GPIVDVPLVINDARVADGTLITLRP-----SDCPHMLVNGKERPYQVAAKRYRF 238

QY 277 RELNAVSRAMLLYLVRTSSPNVRIPFOVIAADGLAPVQTSNLYLAVEREYIIDE 336
DB 239 RYNNACNRYVLRAD-----GIEFQIGDGFLEPRVQSGELMLGSRADIVDF 292
QY 337 TNFAQOTDLRVAENNDG-----EDEYARL--EYKREYVSSGTYEDNSQVSTLRD 389
DB 293 SRY-----KVGDSVLEENQPAQSIERPEVWRFDIV--TAPDVSFVGRLL-- 335
QY 390 VEPPEKGPADKHKFEKERSNGHYLLINDGFADVNERYLAKPELGTVEWMELEN-----SS 445
DB 336 TTYPPQPPYVERDEI--RTFPAMTINGOSY--DPN-RDITAKLTTEYVYKRVNEAPAA 392
QY 446 GG-----WSHPVHILVDFEKLKRTGGRQVMPYESAGLKDVYVLMGRGETLTIEAHYQ 499
DB 393 PGKPDFHLM-HSFHHLTFYRLER--NGKPRAGRDLGKQTYTLGPDVYKIAMTNGP 448
QY 500 WTGAVMHCHNLHEDNDMAVFNVTYA 526
DB 449 YTGQYLHYCHQHGSHSGGMGRIDIVA 475

RESULT 3

QY 08RMC6 PRELIMINARY: PRT: 431 AA.
AC 08RMC6;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Jadz (Fragment).
GN JADZ.
OS Streptomyces venezuelae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=54571;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=ISP5230;
RC MEDLINE=21930291; PubMed=11932454;
RX Wang L., White R.L., Vining L.C.;
RT "Biosynthesis of the dideoxysugar component of jadomycin B: genes in
the jad cluster of Streptomyces venezuelae ISP5230 for L-digitoxose
assembly and transfer to the angucycline aglycone,"
Microbiology 148:11091-1103(2002).
RL EMBL: AY026363; AAL82808.1;
DR NON_TER 431
FT 431
SEQUENCE 431 AA; 47033 MW; 867152A032D1A300 CRC64;

Query Match 16.1%; Score 513; DB 2; Length 431;
Best Local Similarity 33.8%; Pred. No. 4.2e-31;
Matches 155; Conservative 53; Mismatches 195; Indels 56; Gaps 16;
QY 11 ASGLISGLVIGPMDSHPRIEAVDPEVTEVFADSLAAGDDMESPPYNLRYNALPI 70
DB 21 ASGLISRTSL-SDTRAGPGAGSPFAAQPVAQAL-----APITPEFTAPPI 68
QY 71 PVPKOKMITNVPYVGKDIWYIEIIEIKFQORIYPTLRATLVGDMSPGTEVNVPRGT 130
DB 69 PVPARVSVTSTDT-----YSTPVYOTTAELIIPGVATPVLT--YGSFPEPTIKARSGR 121
QY 131 ETVAVFINNATVENSVLHSGSPRAPFDGMAEDVTFPGEYDYVFPNTOSARLLMYHDA 190
DB 122 RVVAKQPRITTTGSMHLGAVVDPBANDGPMDLITPGGRTYTYRPNQVAAATLWYHDA 181
QY 191 FMKTAENAYFGACAGYIINDAEDALGLPSGEGEDIPILITAKKYNADGTL-----RSTE 246
DB 182 HMEAEHYRGMSEGYLLISDNEALPLR--GYDVAIVVRDGLGNDGTLFFDHNTP 239
QY 247 GEDODLMDVYHNGCPMPEFLNVPKRYRFERFLNAAVSRAMLLYLVRTSSPNVRIPFOVI 306
DB 240 GRRS--WS-----TGKQPPYQVAAKRYRLILNGSNRP---EERLSDG---EFTQI 286
QY 307 ASDAGLQAPVQTSNLYLAVEREYIIDFTNF--AGOTDLRNV--AETNDVGDDEYAR 363

Db 287 ASRGLLPARYTTTTLPLSPAERADIVDESRYPVSGSVYLENAYPEPBN----- 337
 QY 364 TLVEMAF-VVSSGTEVDNSOVPSTLRDVPPEPKREGADKHFKFENSGHYLINDVGFAD 422
 Db 338 -KEILRDVYRS--AADPSSVPARLATLPPTAAPTQTRNTLTDFDVGSGSIS--GKTW 392
 QY 423 VNERVLAKPELGTEVWELENSSGMSGSHPIHLYDKFI 461
 Db 393 DEORVDTTVAGDTEWELEKNTHTPEFPHNHILHVDERT 431

RESULT 4

Q9AMU4 PRELIMINARY; PRT; 582 AA.
 AC Q9AMU4: 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 Putative spore coat protein.
 P0044F08.18 OR P0037C04.31.
 Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 NCBI_TaxID=4530;

SEQUENCE FROM N.A.
 RC STRAIN-CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC
 RT clone:P0044F08.18
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 [2]
 SEQUENCE FROM N.A.
 RC STRAIN-CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC
 RT clone:P0037C04.31
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF002909; BAB2118.1; -
 DR EMBL; AF003233; BAB5542.1; -
 DR InterPro: IPR001117; Cu-oxidase.
 DR InterPro: IPR002355; Multicopper oxidase.
 DR Pfam: PF00394; Cu-oxidase; 1
 DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; UNKNOWN_1.
 KW Coat protein.
 SEQUENCE 582 AA; 64050 MW; B5054EECB2C5C1DA CRC64;

Query Match 15.6%; Score 497.5; DB 10; Length 582;
 Best Local Similarity 27.3%; Pred. No. 1e-29;
 Matches 111; Conservative 78; Mismatches 208; Indels 169; Gaps 26;

QY 7 QLAASGLSGVLGIPMDTGSHPTEAVDPEKTEVADSLAAGD-----DWESP-- 59
 Db 6 ELAVLLLVLYGVA-----AGTRPPSAPP-----VVEDTLQKVASLEMYVDELQPKI 55
 QY 60 YNLLYNNALPPIPVYKPKMTITNPYTKDWTYEIEKKPQOKRIPLRPATLYGIDGMS 119
 Db 56 YGFSMRHGHPSP-----IRLTIGMYOKK-WKFRHDL-----PASTVVFVGTG 96
 QY 120 -----PGPTFNPVRGNETVVRFIN-----NATVNSVHLHGSPS 153
 Db 97 AATATTPGPTIEAAGVPLSVTQNTLIPARHILPMDPTVTALIPRRGVTFTVHLLHGGAH 156
 QY 154 RAEFDG-----WAEDVTEPEYKX-----YFPNYOSARLLWYHDAFMKTAENAYF 200
 Db 157 PPGSDSARFAM-----FTAGFGETGPAWSPTTYTYNAOSPGVLWHDHALGLRANLLA 211
 QY 201 GAGGATIIINDEADA-LGLPSGGEFDIPLILAKYNNADGTLRST-----BEGDQ 250
 Db 212 GLGAVAVIRNPFAVEAPLGLPCG--DEFDRLMLADRSFYADGSIYNNYTGIIPIIHQWOP 270

QY 251 DLMGDIVHNGOWPPEFLNVQPRKRYREFELNAASRAWLLYLVRTSPNVRIPROVJASDA 310
 Db 271 EYFEALITVNGKAMPFLAVARRKRIEILINTSNARKNLSITN-----GLPFTVGSDF 324
 QY 311 GLLOAPVQTSNLYLAVEREIIIDFTNFAQOTLDLRNVA-----ETNDVGDEDEYA 362
 Db 325 NYLSKPYTASLAVSAETFDVYVDFSGSSSEAEVNTAPYPYPDQAPNDLNG----- 379
 QY 363 RTLEVMAFVSSGTEVDNSOVPSTLRDVPPEPKREGADKH--FKTE-RSNG---HYLI 415
 Db 380 ---KVMEFVISPAKAKDTSRVPKALDYVAVEEAQVRRIYWEYEDATGNPTHLXY 436
 QY 416 NDVGFADVNERVLAKPELGTEVWELENSSGMSGSHPIHLYDKFIKRG----- 466
 Db 437 NGRLED---PATETPRPGTTEWEYINLTIPD-NHPLHLATFOATRVGLDEDAFKG 492
 QY 467 -----GRGOVWPYESAGIKDVMYLGREGTLT----- 493
 Db 493 CMALKNDVAVGNSVRHVAEGEVAVPEHEKGMKNVYKLAIPYMTIYVKKFFMVDSGRPYF 552
 QY 494 EAHYQPTGAYMMHCHNLIEDNDM 519
 Db 553 DATAEP---GYVYCHILDEHDNAMI 575

RESULT 5

ID 023123 PRELIMINARY; PRT; 568 AA.
 AC 023123;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE F19G10.5 protein.
 GN F19G10.5.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;

SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Federspiel N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway A.R.,
 RA Au M., Araujo R., Buehler E., Dwyer K., Feng C., Li X.,
 RA Oj1 O., Osborne B.L., Shinn P., Sun H., Toriumi M., Vyotskaya V.,
 Yu G., Becker J., Theologis A., Davis R.W.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF000657; AAB72167.1; -
 DR InterPro: IPR001117; Cu-oxidase.
 DR Pfam: PF00394; Cu-oxidase; 1.
 SEQUENCE 568 AA; 64355 MW; C4314C889576E35E CRC64;

Query Match 15.1%; Score 480; DB 10; Length 568;
 Best Local Similarity 28.0%; Pred. No. 2.2e-28;
 Matches 146; Conservative 78; Mismatches 167; Indels 130; Gaps 20;

QY 109 PATLYGIDGMS-----PGTFNPVRGNETVVRFIN-----AT-----V 142
 Db 71 PATPVFAVYGTSSRSKATVPPTIETVYGVVDYVWRNHLIPKSHLLPMDPTISPATPKRGCI 130
 QY 143 ENSVHLHGSPSRAPFDGMADVTPEPEYKX-----YFPNYOSARLLWYHDAFMK 193
 Db 131 PTYVHLHGIGHPTSDGNA-DANFTAGFKETGKRWKTYTLHYENKQDPGMWYHDAFMGL 189
 QY 194 TAENAYFGQAGAYTINDEA-EDALGSPSGGEFDIPLILAKYNNADGTL-RSTEGEDD 251
 Db 190 TRVNLLAGLVAGVILRHHAIVESPQLPTG-DEFDRLIIPDRSPRKDGSIYMATGNPS 248
 QY 252 L-----WGVYHNGOWPPEFLNVQPRKRYREFELNAASRAWLLYLVRTSSPNVRIP 303
 Db 249 IHPQOWPEYGVDAIYVNGKAMPRLNVRARRRIRINASNAREFFKFF-----SNGLDF 302
 QY 304 OVIASDAGLLQAPVQTSNLYLAVEREIIIDFTNFAQOTLDLRNVA-----ETNDVGDE 358

Db 303 IYVSDSAYLSPKATKSTLLSPSEIVDVYDFYKSPSPRTVVLADAPYPGSGPVNNE 362
Qy 359 DEYARTLEVMRFVSSGVEDNSQVSTLRDVPFPKHGKPADKHFKEFR--SNG-----H 412
Db 363 NG-----KVMKFIINNESDDTCTIPKLIINPNADVANAULTRISMEYVSNDEPH 417
Qy 413 YLINDVGF-ADVNERVLAKPELGEVWELENSGGWSPHVIHLVDFKILKRTGGRGV 471
Db 418 LVLNGLPYEAPYTE-----TPKSGTTEVMEVINTLED-NHPLIHILGLFKVEQTA----- 467
Qy 472 MPYESAGLKD-----VVMLGREGTLLIEAHQVPMWG----- 502
Db 468 --LLAAGLEEFKECTKQNDAAVKQISYARCKTAIVTAHERGMKNVFERKMGHVTRILV 525
Qy 503 -----AYMHCHNLIEDNDMAVFN 524
Db 526 RESYHTNATSYPEDPTEGEGYVYHCHILHEDNMAMRPLKV 566

PRELIMINARY; PRT; 581 AA.

Q949X9; 593
AC Q949X9; PRELIMINARY; PRT; 581 AA.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
GN Putative spore coat protein.
OS F23N20.3 OR A1G71040.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
RA Carlini P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamli A., Karlin-Neumann G., Kawai J., Kim C., Kossena E., Lam B.,
RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.,
RA "Full length cDNA of gene F23N20.3 (GI:12323429)".
RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.
[12]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carlini P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamli A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
RA Davis R.W., Ecker J.R., Theologis A.,
RA "Arabidopsis Open Reading Frame (ORF) Clones."
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY050818; AAK92753.1; -
DR EMBL; AY091420; AAM14359.1; -
DR InterPro: IPR001117; Cu-oxidase.
DR Pfam; PF00394; Cu-oxidase; 1.
KW Coat protein.
SQ SEQUENCE 581 AA; 66165 MW; 64873E43FEC24FBD CRC64;

Query Match 14.6%; Score 465; DB 10; Length 581;
Best Local Similarity 28.0%; Pred. No. 3.3e-27;
Matches 142; Conservative 74; Mismatches 182; Indels 110; Gaps 17;

Qy 109 PATLVGYDGM-----PGTFNVPRCTETVVFVFIN-----NATV 142
Db 86 PATVVPALGTSKRSATVPGPTEAVGVDTIVYWRNHLPLHLDPMTISPALPKHGI 145

Qy 143 ENSVHLGGSPSRAPFDGMAEDVTFGEKRD-----YFPNTQASRLMYHDAEMK 193
Db 146 PTVVLHGGIHBPSTDGNA-DSMFTAGFETGSKWTKTTHVVKQOGNMVYHDAAGL 204
Qy 194 TAEANVFOAGYIT-NDAEALALPGSGYGFDPILITAKYAAADGL-RSTGDE-- 249
Db 205 TVVNLGLAGLSYILRHSSVESPLRLPG-REFDEPLIFDRSFKDSIYMAAGNPT 263
Qy 250 -----QDIAGGVIVNGQPPFLVNOPRKYFFRFLNAVSAPMLLYVRTSSPVRIPE 303
Db 264 IHPQMPPEFGDAILVNGKAPRLVYRRKRYFRITNSNAFFRFP-----SNGIDF 317
Qy 304 QVITASDAGILQAPVOTSLYLAVEREITIDTFNFAQOTLDLRNVAETNDVGEDEXAR 363
Db 318 IYVSDSAYLAPKSTSVLAPSEIVLVDFSKSTKTAIANNAPYPSGDPVTE 377
Qy 364 TLEVNRFFVSSGTVEDNSQVSTLRDVPFPKHGKPADKHF--KERENG-----HYLIN 416
Db 378 NSKVMKFTIINKSEVDSTIIPKLTIEP-PAHVSTSTRTTYAMEFYVSSIDEPTLYIN 436
Qy 417 DVGADVERVLAKPELGEVWELENSGGWSPHVIHLVDFKILKRTG----- 466
Db 437 GLPY--NAPVTEPEPKIGSEVMEVINTLED-NHPLIHILGLFKVEQTA----- 492
Qy 467 -----GRGVMPYESAGLKDY-----WLGRETITTE 494
Db 493 MTKRNDAYKCEISKYARGNKTAIVTAHERGMKNVFERKMGHVTKILVRFYSIHNSYSFD 552
Qy 495 AHYOPWTGAYMHCHNLIEDNDMAVF 522
Db 553 ATQEP---GYVHCHILHEDNMAMRPF 577

RESULT 7

Q9FTS3

PRELIMINARY; PRT; 637 AA.

AC Q9FTS3; PRELIMINARY; PRT; 637 AA.
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative spore coat protein-like protein.
GN P0409B08.14.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
NCBI_TaxID=4530;
[1]
RP SEQUENCE FROM N.A.
RA STRAIN-CV. NIPPONBARE;
RC Sasaki T., Matsumoto T., Yamamoto K.,
RA "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:0409B08."
RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF002860; BAB18267.1; -
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; MulticCu-oxidase2.
DR Pfam; PF00394; Cu-oxidase; 1.
DR Prosite; PS00080; MULTICOPPER_OXIDASE2; UNKNOWN1.
KW Coat protein.
SQ SEQUENCE 637 AA; 70919 MW; 692D39F10F2D6A96 CRC64;

Query Match 14.6%; Score 464; DB 10; Length 637;
Best Local Similarity 27.0%; Pred. No. 4.5e-27;
Matches 167; Conservative 83; Mismatches 203; Indels 166; Gaps 27;

Qy 31 EAVDEKTEVEFADSLAAGD---DWESPPVLLYRNALPIPV---KQPKIITN-- 82
Db 48 DSLIPSYICSVISKRWGMASDDPDNDDEYTP-----DHLPLAPAAAGRRRPVMTSLNLT 102
Qy 83 -----PYTGK-----DIWYELIIRKFOQRIY-PTLRPATIV 113
Db 103 KYVDSLPIAKIRGYGIRHGRPVPKILITGMYSKTWOFNHRDMPPTVGVYGOISLOTATF- 161

Db	86	PATPVAYGTGSRKSAATVPSPRTIEAAYGVDTYVTWNNHRLPHLHIIIMPDETISPAPRKAGGI	145
Qy	143	ENSVYHIGSPSRNAPRDCGNAEDVTFPGCEKD-----YFPYQNSRLMYVDHAFMK	193
Db	146	PIYVHLHGSIHEPTSDGNA-DSWFAFGREFGSKWTKTKTTHYVKNQDGNMYDHDHAGL	204
Qy	194	TAEAAFGGACAGYII-NDFAEDALGLPSGCGFIDPLILTAARKYNAODTL-RSTGED--	249
Db	205	TRVNLGLAGLSYILLRHSVESRPLPLPG-REFDRLPIIPDRSRKXOSIYMNATGNPT	265
Qy	250	-----ODIMGDVIHYNQGPFFLVNQPRTKREFRFLNAVSRAMLIVYRTSSPNVRIPF	303
Db	264	IHPQWPEYFGGAIIVNGKAMPRLTVRRKRYKFRITNKSNAFRFRFPF-----SNGIDF	317
Qy	304	OYVASAGLQAPVOTSNIYLAVAREYELIDFTFAQOTLDLNNVAETNDVGDEBYAR	365
Db	318	IYVSGSASIALAPVSTKSYLLAPSELVDLDFESKSTKIALILNNAPIPPSGDPVTEE	377
Qy	364	TLEVMRFVSSGTVEDNSQVPSLTLDVDFPPHKEGPADKH--KFRSNG----HYLIN	416
Db	378	NSKVMKFIINTYKSEVDTSIIIPKLTLP-PAHVSTSTRTRYIAHEVYSSIDEPTHLYIK	436
Qy	417	DVGFADVNERVLAKELGVEVWELENSGSHVHILHLYDFILKRTG-----	466
Db	437	GLPY--NAPVTEPRKIGTSEVWEVINITED-NHPLHILGLFVLDTOLAYKSEETEC	492
Qy	467	-----GRGQVMPRESAGLKDV-----MIGRSETPLIE	494
Db	493	MTRKNDVAVCELSKTKARGKKTAVYHGEKMKVYFMHGHTKILVRFYSIHSNESISFD	552
Qy	495	AHYQPTGAYVMWHCHNLHEDDMXAVP	522
Db	553	ATQEP--GYVYCHILHDEDMXMRPF	577
RESULT 9			
Q9C9A4	ID	Q9C9A4	PRELIMINARY; PRT: 591 AA.
AC	DT	01-JUN-2001 (TREMBLrel. 17, Created)	
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	S309 coat protein-like protein.		
GN	P23N20.3.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eucosids II; Brassicales; Brassicaceae; Arabidopsids.		
OC	NCBI_TaxId=3702;		
RT	[1]		
RA	SEQUENCE FROM N.A.		
RP	STRAIN=CV. COLUMBIA;		
RC	MEDLINE=21016719; PubMed=11130712;		
RA	Theologos A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,		
RA	White O., Alonso J., Altafaj H., Arayo R., Bowman C.I., Brooks S.Y.,		
RA	Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,		
RA	Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,		
RA	Dunn P., Eguu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,		
RA	Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huzar L.,		
RA	Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,		
RA	Kim C.J., Koo H.T., Kremetskaia I., Kritz D.B., Kwan A., Lam B.,		
RA	Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,		
RA	Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzilli A.,		
RA	Millscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,		
RA	Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,		
RA	Sakano H., Salzer S.L., Schwartz J.R., Shinn P., Southwick A.M.,		
RA	Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,		
RA	Utechtack T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,		
RA	Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,		
RT	"Sequence and analysis of chromosome 1 of the plant Arabidopsis		
RT	thaliana."		
RL	Nature 408:816-820(2000).		
RL	EMBL; AC016972; AAG51692.1; -		

DR InterPro: IPR001117; Cu-oxidase.
 DR Pfam: PF00394; Cu-oxidase; 1.
 KW Coat protein.
 SQ SEQUENCE 591 AA; 67358 MW; B0CE7B0E8F05AAF CRC64;

Query Match 14.1%; Score 450; DB 10; Length 591;
 Best Local Similarity 27.4%; Pred. No. 4.8e-26;
 Matches 142; Conservative 74; Mismatches 182; Indels 120; Gaps 18;

QY 109 PATLVGYDGM-----PGTFENVRGTEVYVRFIN-----NATV 142
 DB 86 PATFPAVGTSKRSKRVTPGPTTEAVYGVDTYTMNHLPLHLITLWDPISPAIRKGGI 145
 QY 143 ENSVHLGSPSPAPFDGMAEDVTFPEYKD-----YYPNTQASRLWYHDAEMK 193
 DB 146 PTVVHLHGHIHEPTSDGNA-DSMFTAGFKETGSKTKKTHYVNNQOGNMVYHDAAGL 204
 QY 194 TAEKAVFGQAGYIT-NDEAEDALGPGSGYGFDPILITAKYNAADGL-RSTGED-- 249
 DB 205 TRVNLLAGILGSLYLRHSSVESPLRLPTG-REFDPLVIFDRSFRKDSIYNNATGNNPT 263
 QY 250 -----ODLMDGVHNGOPMPELVNVPKRYFRFLNNAVSRAWLLYLVRTSSPNVRIPE 303
 DB 264 IHPQMPREYFGDAILVNGKAMPRLVYRRKRYFRITMNSNAFFRFF-----SGLDF 317
 QY 304 QVITASDAGILAPVQTSNLYLAVEREIIIDFTNFAQOTLDLRNVAETNDVGDEDEYAR 363
 DB 318 IVVGSDSAYLAKPVSTKSVLLAPSEIVDLVDFSKSTALIANAPYPSPGPTVEE 377
 QY 364 TLEWRFVYVSGTVDNSQVPTLADVPPPHKEPADKH--KERSNG-----HYLIN 416
 DB 378 NSKVKFTLNKSEVDTSIIIPKLLIYP-PAHVSTSTRTRYAMEYVSSIDEPTHLIN 436
 QY 417 DVGFADEVRYLAKPELTVE-----VMELENSGGSHVHLVDFKILKRTG 466
 DB 437 GLPY---NAPYTERPKIGTSEKSLMLTLMKWEVINLTED-NHPLHLHGLFKLEOTA 492
 QY 467 -----GRGOVMPYESAGLKV-----W 484
 DB 493 LVKSEEFTECMTRNDVAKCEISKYARGNKTAFTVHERGKMKVFMGMPGHVTKILVRSY 552
 QY 485 LGRGETLITLHAHYQWPTGAYMKHCHNLHEDNDMAVF 522
 DB 553 IHSNESYSFDAQEP---GYVYHCHILDHEDMMMRPF 587

RESULT 10

067206 PRELIMINARY: PRT: 527 AA.

067206 01-AUG-1998 (TREMblrel. 07, Created)
 01-AUG-1998 (TREMblrel. 07, Last sequence update)
 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Periplasmic cell division protein (SUF1).
 GN SUF1 OR AO_1130.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
 NCBI_taxid=63363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF5;
 RX MEDLINE=98196666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 aeolicus.";
 RL Nature 392:353-358(1998).
 DR EMBL; AE000724; AAC07157.1;
 DR InterPro: IPR001117; Cu-oxidase.
 DR InterPro: IPR002355; Multicu_oxidase2.
 DR Pfam: PF00394; Cu-oxidase; 1.
 DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.

KW Cell division; Complete proteome.
 SQ SEQUENCE 527 AA; 59490 MW; F361BF791FF97355 CRC64;

Query Match 13.8%; Score 439.5; DB 16; Length 527;
 Best Local Similarity 30.1%; Pred. No. 2.6e-25;
 Matches 147; Conservative 72; Mismatches 191; Indels 79; Gaps 21;

QY 98 PQQRITPLRPATLVGYDGMSP-----GPTNVNPGTETVYVFINNATVENS 146
 DB 58 PDGQVSTAKMTTLEVIKGSTDLVYEIDNEYVPIFLKRGQFFSADFVNNSEDSII 117
 QY 147 HLHGPSAPF--DGMADVTFPGYKTYPPN--OSARILMTHDAFMKTAENAVFG 201
 DB 118 HWHG--FRAPWKSDEHPYAAVADGE--TYSYDFTIIDRSGTYFHPHGHGTGYQVYTG 173
 QY 202 QAGAVIINDEADAL--GLPSGYGFDPILITAKYNAADGLRSTEGEDDLDGMDVHV 259
 DB 174 LAGMTIIEDEDDNKQALDLETVIDIPLIQDKTFPSSGQLYNNPGHMGFMQDITLV 233
 QY 260 NGQMPFLNVOPKRYFRFLNNAVSRAWLLYLVRTSSPNVRIPEQVIASDAGLLOAPVQT 319
 DB 234 NLTFRPYMDVERKIRFRILNGSNARPYRALLR--GNQRYRFVYVIGEGGLDTPREV 290
 QY 320 SNLYLAVEREIIIDFT-----NFAQTLDL-----RNAETN--- 353
 DB 291 NEILVAPGERIDIIVDFDASVNDVYIKLYNPNHNLIGMIGMRMGMEKMGNGMN 350
 QY 354 -DVG--DDEYARTLEWRFVYVSGTVDNSQVPTLADVPPPHKEPADKHFEKERSN 410
 DB 351 MDGMADNSEF---EVMERFVTKDSAYDKS-IPRLSEVT-PINTDAQOVRITLGR 404
 QY 411 GHYLIN---DVGFA--DVNE-RVLAPELTGVEWELSENSGGSHVHLVDFKIL 462
 DB 405 MYFTINGETWEDGANPDINNPKVLFQNGNDVYIIEYVNTGMV-HPMHIGHQFQVL 463
 QY 463 KRTGGRGOVMPYESA--GLKDVYMLGKRETLTIE--AHQWPTGAYMKHCHNLHEND 517
 DB 464 ERSIG-----PLRATDGMKDTVIAPMETVRIADVMSHPYNEHOIYLLHCHLHEDG 518
 QY 518 MAAVENYTA 526
 DB 519 MAAVTRYNA 527

Search completed: July 1, 2003, 10:41:00
 Job time : 91 secs

GenCore version 5.1.6
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6388329

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 3, 2003, 22:08:06 ; Search time 4358 Seconds

(without alignments)
3966.743 Million cell updates/sec

Title: US-10-080-233-2

Perfect score: 3189
Sequence: 1 MLEKSMQLAAAGSLSGVLG.....AEOPEYNRIDELLEDGIEE 594

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DEV=rlh
-Q=/cgn2_1/uspt0.spool/US10080233/runat_01072003_094519_26096/app.query.fasta_1.775
-DB=GenEmbl -QFMT=fastap -SUFFIX=trge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORE=pep -THR.MAX=100 -THR.MIN=0 -ALIGN=10 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10080233 -GCN1_1.2818 -gcunat_01072003_094519_26096 -NCPU=6 -ICPU=3
-NO_MAP -LANG=BOUERR -NEG.SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl: *
2: gb_hlg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_da: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
29: em_vl: *	3189	100.0	1791	6 AR211556	AR211556 Sequence
30: em_hlg_hum: *	3165	99.2	7259	6 AX384798	AX384798 Sequence
31: em_hlg_hum: *	3056	95.8	3672	6 AR211554	AR211554 Sequence
32: em_hlg_other: *	1870	58.6	2063	6 AR211555	AR211555 Sequence
33: em_hlg_mus: *	1868	58.6	2905	6 AR211555	AR211555 Sequence
34: em_hlg_pin: *	1724.5	54.1	1942	8 MYRBOR	D12579 M. verrucar
35: em_hlg_rod: *	1724.5	54.1	1959	6 E05283	E05283 B11rubi o
36: em_hlg_mam: *	1708.5	53.6	2126	6 AR122996	AR122996 Sequence
37: em_hlg_vrt: *	1620.5	50.8	1958	6 AR122996	AR122996 Sequence
38: em_sy: *	1620.5	50.8	1958	6 AX108672	AX108672 Sequence
39: em_hlg_hum: *	1620.5	50.8	1958	6 AX108672	AX108672 Sequence
40: em_hlg_mus: *	1620.5	50.8	1958	6 AX108672	AX108672 Sequence
41: em_hlg_other: *	1620.5	50.8	1958	6 AX108672	AX108672 Sequence
42: em_hlg_hum: *	1620.5	50.8	1958	6 AX108672	AX108672 Sequence
43: em_hlg_mus: *	1620.5	50.8	1958	6 AX108672	AX108672 Sequence
44: em_hlg_other: *	1620.5	50.8	1958	6 AX108672	AX108672 Sequence
45: em_hlg_hum: *	1620.5	50.8	1958	6 AX108672	AX108672 Sequence

RESULT 1

ALIGNMENTS

AR211556	AR211556	1791 bp	DNA	linear	PAT 20-JUN-2002
LOCUS					
DEFINITION	Sequence 5 from patent US 6399329.				
ACCESSION	AR211556				
VERSION	AR211556.1	GI:21514909			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1791)				
TITLE	Wang, H. and Bodie, E.A.				
JOURNAL	Phenol oxidizing enzymes				
FEATURES	Patent: US 6399329-A 5 04-JUN-2002;				
	Location/Qualifiers				
Source	1..1791				
	/organism="unknown"				
BASE COUNT	360 a	551 c	451 g	409 t	
ORIGIN					

Alignment Scores:

Seq. No.:	1.04e-247	Length:	1791
Score:	3189.00	Matches:	594
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-080-233-2 (1-594) x AR211556 (1-1791)

QY	1	MettLeuPheLysSerTropInLeuAlaAlaSerGlyLeuLeuSerGlyValLeuGly	20
Db	7	ATGCTGTTCAAGTCAATGGCAATGGCAGCAAGCTCCGGGCTCTGTGTGGAGCTCGGC	66
QY	21	ILleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu	40
Db	67	ATCCGATGAGAACACCGGCAGCCACCATTGAGGGCTGTGATCCGACGAGGAGACTGAG	126
QY	41	ValPheAlaAspSerLeuLeuAlaAlaGlyAspAspAspTrpGluSerProProTyr	60
Db	127	GCTCTCGGTGACTCCCTCCCTTCGTGAGGAGGCGAGAGACACTGGGAGTCACTCCATAC	186
QY	61	AsnLeuLeuTyrArgAsnAlaLeuProIleProValLysGlnProLysMetIleIle	80
Db	187	AACTTGCTTACAGGAATGCCCTGGCAATTCCACCTGTCAAGCAGCCCAAGATGATCATT	246
QY	81	ThrAsnProValThrGlyLysAspIleTyrTyrGluIleGluIleLysProPheGln	100
Db	247	ACCAACCCGTGCACCCGCGAGACAACTTGTTACTATGAGATGCAGATCAAGCCATTTCAG	306
QY	101	GlnArgIleTyrProThrLeuArgProAlaThrLeuValGlyTyrAspGlyMetSerPro	120
Db	307	CAAAAGATTACCCACCTGGCGCCCTGGCACTCTGTGGCTACGATGGCAATGACCCCT	366
QY	121	GlyProThrPheAsnValProArgGlyThrGluThrValValAlaPheIleAsnAla	140
Db	367	GGCTCACTTTCATGATGTCCCGAGAGGAACAGAGACTGTAGTTACATCAACAAATGCC	426
QY	141	ThrValGluAsnSerValHisLeuHisGlySerProSerArgAlaProPheAspGlyTrp	160
Db	427	ACCGTGGAGAACTCGCTCATCTGCACGGCTCCCACTCCGTCGCCCTTTCGATGGTTGG	486
QY	161	AlaGluAspValThrPheProGlyGluTyrLysAspTyrTyrPheProAsnTyrGlnSer	180
Db	487	GCTGAGAGTGTGACTTCCCTCGCGAGTCAAGAGATTACTACTTTCACACTACCAATCC	546
QY	181	AlaArgLeuLeuTyrTyrHisAspHisAlaPheMetLysThrAlaGluAsnAlaTyrPhe	200
Db	547	GCCCGCCTTCGTGTGATCATGACACACGCTTCATGAAAGACTGCTGAGATGCTCACTT	606
QY	201	GlyGlnAlaGlyAlaTyrIleIleAsnAspGluAlaGluAspAlaLeuGlyLeuProSer	220
Db	607	GGTCAAGCTGGGGCTTACATTATTCACGACGAGGTGAGAGATGCTTCGCTCTCTCAAGT	666

QY	221	GIYTRGIYGLINPheAspLIleProeuLIleuThrAlaLYSTYTYrAsnAlaAspLI	240
Db	667	GGCTATGGCGAGTTCGATATCCCTCGATCCGAGCGCAAGTACTATTAAGCCGATGT	726
QY	241	ThrLeuArGserThrGIuGLIuAspLIAspLeuTrpGIAspValIleHisValAsn	260
Db	727	ACCGTGGCTTGACCGAGGCTGAGGACCAAGACCTGTGGAGATGATCATGATCAAC	786
QY	261	GLYGIInProTrpProPheLeuAsnValInProArgLYSTYrArGpHeArGpHeLeuAsn	280
Db	787	GGACAGCCATGGCCCTTTCCTTAACGTCCAGCCCGCAAGTACCGCTTCCGATTCCTCAAC	846
QY	281	AlaAlaValSerArgAlaIleTrpLeuLeuLYrLeuValArgThrSerSerProAsnValArg	300
Db	847	GCTGGCGGTCTCGGCTTGGCTCTCTACTCTGTCAAGACAGCTCTCCCAAGCTCGA	906
QY	301	IleProPheGIInValIleAlaSerAspAlaLYleuLeuGIInAlaProValGIInThrSer	320
Db	907	ATTCCTTCCAAAGTCATTTGGCTCTGATCTGTCTCTCTTCAAGCCCGCTTCAGACCTCT	966
QY	321	AsnLeuLYrLeuAlaValAlaGLuArgTYrGIuIleIleLeaSPheThrAsnPheAla	340
Db	967	AACCTCTACCTGTGCTGTGGCGAGCGGTACAGATCATTAATGACTTCACCAACTTTCCT	1026
QY	341	GIYGIInThrLeuAspLeuArgAsnValAlaGIInThrAsnAspValGIYAspLIuAspLI	360
Db	1027	GGCCGAGACTCTGAGCTCGCAACTGCTCGAGCAACGATGTGGCGAGAGAGATAG	1086
QY	361	TYrAlaArGThrLeuGIuAlaMetArgPheValValSerSerGIYThrValGIuAspAsn	380
Db	1087	TACGCTGCACCTCTGAGGTGATGGGCTCGTCGTCACTCTGGGACTGTTGAGAGAAC	1146
QY	381	SerGIInValProSerThrLeuArgAspValProPheProHisLYSGLIYProAla	400
Db	1147	AGCCAGGTCCTCCCTCACACTCTCGTGACCTTCCTTCCCTCCCAAGAGAGCCGCCCC	1206
QY	401	AspLYSHISpHeLYsPheGIuArgSerAsnGIYHisTYrLeuIleAsnAspValGIYpHe	420
Db	1207	GACAAAGCACTTCAGTTGAAAGCGCAGCAAGGACATCACTGATCAACGATGTGGCTTT	1266
QY	421	AlaAspValAsnGLuArgValLeuAlaLYsProGIuLeuGIYThrValGIuValTrpLIu	440
Db	1267	GCCATGTGCATGAGCCGTCTCTGGCCAAAGCCGAGCTGGCACCCGTTGAGTCTGGAG	1326
QY	441	LeuGIuAsnSerSerGIYLYrTrpSerHisProValHisIleHisLeuValAspPheLYs	460
Db	1327	CTCGAGACCTCCTCTGAGAGCTGGAGCCACCCGCTCCATTCACCTGTTGACTTCAAG	1386
QY	461	IleLeuLYsArgThrGlyGIYArgGIYInValMetProLYrGIuSerAlaGLYLeuLYs	480
Db	1387	ATCTTCAGACGAACTGTGTGTGTGGCCAGGTCAATGCCCTCGAGTCTGTGGTCTTAAG	1446
QY	481	AspValValTrpLeuGIYArgGIYGIuThrLeuThrIleGIuAlaHisTYrGIInProTrp	500
Db	1447	GATGTCTGTGGTGTGGAGGGGTAGACCTTGACCATTCGAGGCCCTACCAACCTCTGG	1506
QY	501	ThrGIYAlaTYrMetTrpHisCYsHisAsnLeuIleHisGIuAspAsnAspMetMetaIa	520
Db	1507	ACTGAGAGCTTACATGTGGCACTGTACAACTCATTCACGAGGATTAACGACATGATGCT	1566
QY	521	ValPheAsnValThrAlaMetGIuGLYsGLYrTYrLeuGIInAspPheGIuAspPro	540
Db	1567	GTATTCACAGTCACCGCCATGGAGAGAAAGGATATCTTCAGGAGGACTTCGAGAGCCCC	1626
QY	541	MetAsnProLYsTrpArgAlaValProLYrAsnArgAsnAspPheHisAlaArgAlaGLY	560
Db	1627	ATGAACCCCAAGTGGCGGCGCTTCCTTACAAACGCAACGACTTCATGCTCGCGCTGGA	1686
QY	561	AsnPheSerAlaGIuSerIleThrAlaArgValInGIuLeuAlaGIuGIInGIuProLYr	580
Db	1687	AACCTTCTCGCCGAGTCCATACACGTCCCGAGTGCAGAGCTGGCCGCAAGACCGCTAC	1746
QY	581	AsnArgLeuAspGIuIleLeuGIuAspLeuGIYIleGIuGIu	594

QY 540 romelasnprolystpralalavalprotyrasnargasnasphehisalargalag 560
| | | | |
Db 6827 CCATACACCCAGAGGCGCGCGCTTCTACAAACCGACAGACTTCCATGCTCCGCTG 6886
QY 560 lyaaspheSerAlagIuSerIlethrAlaargValGInGluLeuAlaGInGInGInuprot 580
| | | | |
Db 6887 GAACATCTCCGCGAGTCATCACTGCGCCGAGTcAGAGAGCTGGCCAGAGCAGAGCGCT 6946
QY 580 yrasnargLeuaspGluIleLeuGluaspLeuGlyIleGluGlu 594
| | | | |
Db 6947 ACAACCGCTCGATGAGATCTCGAGGATCTTGATGATGAGAGAG 6990
RESULT 3
AR211554 3677 bp DNA linear PAT 20-JUN-2002
LOCUS AR211554
DEFINITION Sequence 1 from patent US 6399329.
ACCESSION AR211554
VERSION AR211554.1 GI:21514906
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3677)
AUTHORS Wang, H. and Bodle, E. A.
TITLE Phenol oxidizing enzymes
JOURNAL Patent: US 6399329-A 1 04 -JUN-2002;
FEATURES Location/Qualifiers
source 1. 3677
/organism="unknown"
BASE COUNT 822 a 1057 c 849 g 948 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 1.36e-236 Length: 3677
Score: 3056.00 Matches: 593
Percent Similarity: 86.70% Conservative: 0
Best Local Similarity: 86.70% Mismatches: 1
Query Match: 95.83% Indels: 91
Gaps: 5
US-10-080-233-2 (1-594) x AR211554 (1-3677)
QY 1 MetleuphelysSerTrpGlnLeuAlaAlaAspSerGlyLeuSerGlyValIleuGly 20
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Db 1044 ATGCTGTCAAGTATGCACTGGACACACCTCCGGCTCTGCTGAGATCCTCGGC 1103
QY 1 IlePrometAspThrGlySerHisProIleGluAlaValaspProGluValIlyThrGlu 40
| | | | |
Db 1104 ATCCCGATGACACCGGACGCCACCCCAATGAGGCTGTGATCCCGAAGTGAAGACTGAG 1163
QY 41 ValPheAlaaspSerLeuLeuAlaAlaAlaGlyaspAspAspTrpGluSerProTyr 60
| | | | |
Db 1164 GTCTTCGCTGACTCCCTCTTCTGTCAGACAGGCGATGACGACTGGATCTACCTCCATAC 1223
QY 61 AsnLeuLeu-----Tyr 64
| | | | |
Db 1224 AACTTGCTTTACAGGTGAGACACCTGTCCACCTGTTTTCCCTGATTAACCTAATCTTAT 1283
QY 65 ArgasnAlaLeuProIleProProValIysGlnProIlyMet----- 78
| | | | |
Db 1284 AGGAATGCCCTGACCAATTCACCTGTCTCAAGCAGCCCAAGATGATGTCTTGAATTTCTTA 1343
QY 79 -----IleIleThrAsnProValThrGly 87
| | | | |
Db 1344 CGAAGCAACTGCGCCGACACTAATGATATTAGATCTTACCAACCTGTCCACCGGAA 1403
QY 87 sasPileTrpTyrTrpGluIleGluIleIysProIleGlnIleArg----- 102
| | | | |
Db 1404 GGACATTTGTGACTATGATGATGATGATCAACGCAATTCACGAAAGGAGTGTGCTCAG 1463
QY 103 -----IleTyrProThrLeuArgPr 109
| | | | |
Db 1464 AAACCTGTGTAAATTAATCATTTGTTACTGACCTTTTCAGATTTACCCACCTTGCGGCC 1523

QY 109 oAlaThrLeuValGlyTyrAspGlyMetSerProGlyProThrPheAsnValProArgGly 129
| | | | |
Db 1524 TGCCACTCTCGTCCGCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1583
QY 129 yThrGluThrValAlaArgPheIleAsnAsnAlaThrValIleuAsnSerValHisLeuH 149
| | | | |
Db 1584 AACAGAGACTGTAGTTCATCAACAAAGCCACCTGGAGAACTCGTCCATCTGCA 1643
QY 149 sGlySerProSerArgAlaProPheAspGlyThrAlaGluaspValThrPheProGly 169
| | | | |
Db 1644 CGGCTCCCATCGCGTGGCTTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1703
QY 169 uTyrIlyAspTyrTyrPheProAsnTyrGlnSerAlaArgLeuLeuTrpIlyHisAspH 189
| | | | |
Db 1704 GTACAGAGATTAACACTTCTCCCACTACCAATCCGCCCTTCTGTGTGATGATGATGATGATGAT 1763
QY 189 sAlaPheMetIly----- 193
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Db 1764 CGCTTTCATGAA -GGTATGCTACGAGCCTTATCTTCTGCTACCTTTGGCTAACCA 1822
QY 194 -----ThrAlaGluaspAlaTyrPheGlyGlnAlaGlyAlaTyrIleIleAs 209
| | | | |
Db 1823 CTTCCTTTCGTAGACTGCTGAGAAATGCTTACTTGTGCTAGGCTGGCGCTACATTAACAA 1882
QY 209 nasPgluaIaGluaspAlaLeuGlyLeuProSerGlyTyrGlyGluPheAspIleProle 229
| | | | |
Db 1883 CGACGAGGCTAGAGATGCTCGGCTCTTCAGTGGCGATGCGAGTTCGATTCCTCT 1942
QY 229 uIleLeuThrAlaIlyTyrTrpAsnAlaAspGlyThrLeuArgSerThrGluGluAs 249
| | | | |
Db 1943 GATCCTGACGCGCAAGTACTTAACGCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 2002
QY 249 pGlnaspLeuTrpGlyaspValIleHisValAsnGlyGlnProTrpPheLeuAsnVa 269
| | | | |
Db 2003 CCAGGACCTGTGGGAGATGTCATTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 2062
QY 269 lGlnProArgIlyTyrArgPheArgPheLeuAsnAlaAlaValSerArgAlaTrpLeu 289
| | | | |
Db 2063 CCAGCCCGCAAGTACGCTTCGATTCCTCAAGCGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2122
QY 289 uTyrIleuValArgThrSerSerProAsnValArgIleProPheGlnValIleAlaSerAs 309
| | | | |
Db 2123 CTACCTGCTCAGGACAGCTCTCCCAACGTCAGATTCCTTCCAAAGTCATTTGCTCTGTA 2182
QY 309 pAlaGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyrTrpLeuAlaValaGluAr 329
| | | | |
Db 2183 TGTGCTCTCTTAAGCCCCCGTTCAAGCTCTTAACCTTAACCTTCTGCTGCTGCTGCTGCTGCTGCT 2242
QY 329 gTyrGluIleIleIle----- 334
| | | | |
Db 2243 TTACGAGATCAATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2302
QY 335 -----AspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaGly 351
| | | | |
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QY 351 uThrAsnAspValGlyaspGluaspGluTyrAlaArgThrLeuGlnValMetArgPheVa 371
| | | | |
Db 2363 GACCAAGATGTCGCGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2422
QY 371 lValSerSerGlyThrValGluaspAsnSerGlnValProSerThrLeuArgaspValPr 391
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QY 391 oPheProProHisIlysgIuGlyProAlaAspIlyHisPheIlyspheGluArgSerAsnGly 411
| | | | |
Db 2483 TTTCCTCTCTCACAAGAGAGCCCGCGCAACACTTTCAGATTTCAAGCAGCAGCAACG 2542
QY 411 yHisTyrLeuLeuAsnAspValGlyPheAlaAspValAsnGluArgValIleuAlaIlySpr 431
| | | | |
Db 2543 AACACTACCTGATCAAGATGTTGCTTGGCAGATGTCAAATGAGGCTGCTGCGCAAGCC 2602

QY 334 IleAspPheThrAsnPheAlaGlyIleThrLeuAspLeuArgAsnValAlaGlyIleThrAsn 353
Db 1194 TTCGACTTTCGCCCTTATGACAGCCAGATGATGTTGGCTTAACCTTTCACAAAGGCCAAT 1253
QY 354 AspValGlyAspGluAspGluTyrAlaArgThrLeuGluValMetArgPheValSer 373
Db 1254 GGGGTGCGCAGCAGATGATGATATGCAACACTGCAACAGTATCGGCTCATCTCAAC 1313
QY 374 SerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspValProPhePro 393
Db 1314 AGCCAAGACGTGCTGATACCTGGTGTACCCGACAGCTATCTCAGATTCAGTTCCCC 1373
QY 394 ProHisGlyGluGlyProAlaAspLysHisPheLysPheGluArgSerAsnGlyHisTyr 413
Db 1374 GCCGCAAAACCCGGC---ATGCAACCACTCCCTCCATCGCACCACAGCCAGTGG 1430
QY 414 LeuIleAsnAspValGlyPheAlaAspValAsnGluArgValLeuAlaLysProGluLeu 433
Db 1431 CGCATCAACGGCATGGGTTTGCACAGCTCCAGAACCGTATCTGCGCAAGTACCGCGC 1490
QY 434 GlyThrValGluValTyrGluLeuGluLysAsnSerSerGlyGlyTyrSerHisProValHis 453
Db 1491 GGCACGTGCGAGCTATGGAACTCGAAGAACCTCGGGGGCTGTGCGACCCCATTCAC 1550
QY 454 IleHisLeuValAspPheLysIleLeuLysArgThrGlyGly-----ArgGlyGln 470
Db 1551 GCCACCTGTGCTGCTCGAGTCCGAGTCTCGACGCTGAGTGCAGCAAGCACTCGCGC--- 1607
QY 471 ValMetProTyrGluSerAlaGlyLeuLysAspValValTyrPheGluValArgGlyGluThr 490
Db 1608 GTCAAGCCCTACAGATCCGCGCGCTCAAGAGACGTGCTGTGCTGCGCGCCACAGACG 1667
QY 491 LeuThrIleGluAlaHisTyrGlnProTyrThrGlyAlaTyrMetThrPheHisCysHisAsn 510
Db 1668 GTGCTGCTGCAAGCAGCTACGCGCCCGTGGAGAGTCAATGATGTCACATGCGACAC 1727
QY 511 LeuIleHisGluAspAsnAspMetMetAlaValPheAsnValThrAlaMetGluLys 530
Db 1728 CTGATCCAGCAAGACCAATGATGGCCGCTTTCAGTCACTCAACCTCCAGAACTTT 1787
QY 531 GlyTyrLeuGln---GluAspPheGluAspProMetAsnProLysTyrArgAlaValPro 549
Db 1788 GGGTCAACAGACAGCAGATTTCCACAGACCCGGAAGATTCGCTGCTGTCAGACACC 1847
QY 550 TyrAsnArgAsnAspPheHisAlaArgAlaGluAsnPheSerAlaGluSerIleThrAla 569
Db 1848 TTCACCGCGCGCTGATGACGCGGATGCGGATATCTCTCAGAGCATCCATCAGGGCT 1907
QY 570 ArgValGlnGluLeuAlaGluGlnGluProTyrAsnArgLeuAspGluIleLeuGlnAsp 589
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QY 590 Leu 590
Db 1968 CTC 1970

RESULT 5
AR211555 2905 bp DNA linear PAT 20-JUN-2002
LOCUS AR211555
DEFINITION Sequence 3 from patent US 6399329.
ACCESSION AR211555
VERSION AR211555.1 GI:21514907
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2905)
AUTHORS Wang, H. and Bodie, E. A.
TITLE Phenol oxidizing enzymes
JOURNAL Patent: US 6399329-A 3 04-JUN-2002;
FEATURES 1. 2905
Location/Qualifiers
Source /organism="unknown"

BASE COUNT 714 a 792 c 664 g 734 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 5,55e-141
Score: 1868.00 Matches: 2905
Percent Similarity: 67.82% Conservative: 81
Best Local Similarity: 55.59% Mismatches: 132
Query Match: 58.58% Indels: 83
DB: 6 Gaps: 10
US-10-080-233-2 (1-594) x AR211555 (1-2905)
QY 2 LeuPheLysSerTyrPheGluAlaAlaAlaSerGlyLeuSerGlyValLeuGlyIle 21
Db 129 CTCTTCGACGACTTCACACTCGTTCA-----ATTGGGAAGGATATACGGTGC 179
QY 22 ProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGluVal 41
Db 180 GCTTTG-----AGCAACGTCCCGCAAAATTTGTGCAACACCCCGACGAAGAAAG 233
QY 42 PheAlaAspSerLeuAlaAlaAlaGlyAspAsp----- 53
Db 234 GCTGCC-----TTGGCTCAATTGTGAAGATGACCTCGGAGTGTGTCAACATGCTG 287
QY 54 ---AspTyrPheGluSerProTyrAsnLeuLeuTyrArgAsnAlaLeuProIleProPro 72
Db 288 AAAGACTGGCAAAAGCCGAGATATCTCATTTTTCGCAACACATCCCATCCATCCCA 347
QY 73 ValLysGlnProLysMetIle----- 79
Db 348 GCCAAGGAACCAAGTA-GTAGTGTTCATATCGCATGACAGCTTTCTTAAATATATCTC 406
QY 80 -----IleThrAsnProValThrGlyLysAspIleTyrTyrGlyIle 94
Db 407 ACCATCCACAGTAAACTACAGATCTCTCAACAAAGAGATATGTTACTAGAGATT 466
QY 95 GluIleLysProPheGlnAlaArgIleTyrProThrLeuArgProAlaThrLeuValGly 114
Db 467 GTCATCAAAACCTTCACCCAGCAGAGTATGATCAAGACCTCGCGCTGTAGTAGAGC 526
QY 115 TyrAspGlyMetSerProGlyProThrPheAsnValProArgGlyThrGluThrValVal 134
Db 527 TATGACGGCATCTCCCGAGTCTCAATCATAGTACGGAAGGAAGAAAGCTGTGTGA 586
QY 135 ArgPheIleAsnAsnAlaThrValGluLysSerValHisLeuHisGlySerProSerArg 154
Db 587 CGGTTATATAACAGAGGTGATCGGGAAGCTCATCTCCACGGCTCCCGCTCCCGT 646
QY 155 AlaProPheAspGlyTyrAlaGluAspValThrPheProGlyGlyTyrLys----- 171
Db 647 GCCCTTTTGACGAGTGGGTGATGATGATCATGAAGGGGGAATACAA-AGGTACGAT 705
QY 172 -----Asp 172
Db 706 AGCGTGTATCTTACGCAATCAAGAACCTTATATCACTAACAAGACTTTTCTTCACAG 765
QY 173 TyrTyrPheProAsnTyrGlnSerAlaArgLeuTyrTyrHisAspHisAlaPhe-Me 192
Db 766 TACTACTACCCGAAACCAACCAAGCTGCCAGATTTTGTGTGCCACAGATCATGCTATGAT 825
QY 192 t----- 192
Db 826 GTTGAAGTCTTTACCGCACTTTTCATGTAGTGAAGGAAGATTAAGTAAACATCTGT 885
QY 193 -LysThrAlaLysAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleIleAsnAspGluAl 212
Db 886 GCAGACCGCAGAAAATGCTATTTTCGGCAAGCCGGCGCTTACGATACACACCGCGC 945
QY aglAspAlaLeuGlyLeuProSerGlyTyrGlyGluPheAspIleProLeuIleLeuTh 232
Db 946 TGAGGATGCTCTCGGCTTCTTCAAGGTACGGAAATATACACATTCGCTGCTCAG 1005

OY	232	AlaLysTyrTyrAsnIlaSpGIYThrIleuArgSerThnGluIuGIuAspIle	252
Db	1006	TTCCAAgTACTACAAcCGGATGGAACTCTTAAGACCAAGTGGGAAGACCAAGAGTGT	1065
OY	252	uTrpGlyAspValIleHisValaenGIgnProTrpProPheIleuAsnValGlnProAr	272
Db	1066	TTGGGGGGAACATCATTCATGTCACAGGTCAGCCCTGGGCATTTCTTAATGTGAGCCTCG	1125
OY	272	gLySTyrArgPheArgPheIleuAsnIlaIaValSerArgIaIaTrpIleuTyrLeuVa	292
Db	1126	AAAGTATCGTCTTGATTCCTCAACGGCGGCTGTTCAGGAACCTTGCCCTTACTTCGT	1185
OY	292	LaArgThrSerSerProAsnValaArgIleProPheGlnValIleIaSerAspIaGlyLe	312
Db	1186	CAACCAAGACAAcTGTCCACTAGGCTTCCTTCACAGTCATTCCTCTGATGGAGGGCT	1245
OY	312	uLeuGlnIaIaProValGlnThrSerAsnLeuTyrLeuAlaValaIaGluArgTyrGluI	332
Db	1246	ACTCAACACACCCGGTTCAACCTAGATATGTATGTTCGACCCGACAGCCTTACAGAT	1305
OY	332	eIleIleAspPheThrAsnPhenIaGlyGlnIleuAspLeuArgAsnValaIaGluTrh	352
Db	1306	TGTGTGTGATTTCCGCCGCTATGCCGGCAAAACCTTGATCTGGCAACTTCGAAAGGC	1365
OY	352	rAsnAspValGlyuAspGluAspGluTyrIlaIaArgThrLeuGluIuValaIaMetArgPheVala	372
Db	1366	CAATGGATCGGTACCGACGACGACTACGCAAAACAGCAAGGTCAATGGCTTCCACGT	1425
OY	372	IserSerGIYThrValGluAspAsnSerGlnValProSerThreuArgAspValProPh	392
Db	1426	CAGCAAGCCAAACAGTCTGTCATCTCGTGTCACCCGACGACTATCTCAGATCCAGTT	1485
OY	392	eProProHisIleuGluIuProIaAspLysHisPheLysPheGluIuSerAsnGluIuH	412
Db	1486	CCCCGGGACAAAC---GACATAGACATCACTTCGCTTCATCGTACGTCACAAAGCGGA	1542
OY	412	sTyrLeuIleAsnAspValGlyPheIlaIaAspValaIaAsnGluArgValaIleuAlaLysProGI	432
Db	1543	GTTGGCGCATCAACGGCATCGGGTTTGAGAGCTGGAGAACCGTCTTGTGCCAAGGTACC	1602
OY	432	uLeuGIYThrValaIuValTrpGIuLeuGluAsnSerSerGIYGlyTrpSerHisProVa	452
Db	1603	GGCGGGTACTCTCAGCTTGTGGAACTTGAGAACAGCTCCGGCGGGCTGTGCACACCCAT	1662
OY	452	IHisIleHisLeuValaAspPheLysIleLeuLysArgThrGIYIaArgIeGIgn-----	470
Db	1663	CCAGCTGCACACTAGTAGCTTCGAGTGTGCAGCGGTAGCGGCACGAAGCACTCGCGG	1722
OY	471	-ValMetProTyrGIuSerIaGlyLeuLysAspValaValaTrpLeuGIYArgGIYIuTh	490
Db	1723	CGTCAATCCCTATAGGCGCGCGGTCTCAAGAGAGCTGTGGCTCGCGCTGCAGAGAC	1782
OY	490	rLeuThrIleGluIuIaHisTyrGlnProTrpThrGIaIaTyrMetThrPHisCysHisAs	510
Db	1783	GGTCTCTGTGCAGACATTTACGCCCCATGGGAGCGAGTCTACATGTCTCCACGTCCACAA	1842
OY	510	nLeuIleHisIaGluAspAsnMetMetIaValaIaPheAsnValaIaIaMetGIuGIuLy	530
Db	1843	CCATCATCCAGAACACAAAGCAGCATGATGGCGGCTTGAGGTGACTTAACCTCCAGAACTT	1902
OY	530	sGIYTYrLeuGIgn---GluAspPheGIuAspProMetAsnProLysTrpArgIaValaIaPr	549
Db	1903	TGGGTACAAAGAGGAGTGTTCACAGATCCCTGAGAGATCTCGTGTGCACGAAGACC	1962
OY	549	oTyrAsnArgAsnAspPheHisIaIaArgIaGlyAsnPhSerArgIaIuSerIleThrAl	569
Db	1963	TTTACCGCGGGTATCTCACGGCGCATGGGATCTTTTCACAAAGATTCATCACAGGC	2022
OY	569	aArgValaGlnIuLeuIaGluGlnIuProTyrArgAsnArgLeuAspGIuIleLeuGIuAs	589
Db	2023	TAGAGTAAAGAGTGGGGCGTCCAGACAGCCTTACAGGCACTGCCACAAGTTCAGCCTC	2082
OY	589	pLeu 590	

DB	2083	GCTC	2086	111
RESULT 6	MYRBOR			
LOCUS	M. verrucaria mRNA for bilirubin oxidase, complete cds.	1942 bp	mRNA	linear
DEFINITION				PLN 01-FEB-2000
ACCESSION	D12579			
VERSION	D12579.1	GI:456711		
KEYWORDS	bilirubin oxidase.			
SOURCE	Myrothecium verrucaria (strain:MT-1) cDNA to mRNA.			
ORGANISM	Myrothecium verrucaria			
REFERENCE	Eukaryota, Fungi; Ascomycota; mitosporic Ascomycota; Myrothecium. 1 (bases 1 to 1942)			
AUTHORS	Kolkeba, S., Ando, K., Kajih, H., Inoue, T., Murao, S., Takeuchi, K. and Samejima, T.			
TITLE	Molecular cloning of the gene for bilirubin oxidase from Myrothecium verrucaria and its expression in yeast			
JOURNAL	J. Biol. Chem. 268 (25), 18801-18809 (1993)			
MEDLINE	93366794			
REFERENCE	2 (bases 1 to 1942)			
AUTHORS	Ando, K.			
TITLE	Direct Submission			
JOURNAL	Submitted (07-JUL-1992) Keiichi Ando, Amano Pharmaceutical Co., Ltd., Tsukuba Research Laboratories; 22 Miyukiyaoka, Tsukuba, Ibaragi 305, Japan (Tel:0298-56-5026, Fax:0298-56-5012)			
COMMENT	On Feb 26, 1994 this sequence version replaced gi:436235. Submitted (07-JUL-1992) to DDBJ by: Keiichi Ando			
FEATURES				
SOURCE	0298-56-5026 0298-56-5012. Location/Qualifiers 1..1942 /organism="Myrothecium verrucaria" /strain="MT-1" /db_xref="taxon:5532" 66..1184 /EC_number="1.3.3.5" /codon_start=1 /product="bilirubin oxidase" /protein_id="BA02123.1" /db_xref="GI:456712" /translation="MERHTUGAALLSLFNSNAVQASVPETSPATGHLKRRVAQISPP QYPMETVPLIPYKQRLVTNPNQCEITWYVEVETKPEFHQVYPLDGSADLVGYDGG MSPEPTQVPGVETVYVREINNAEAPNSVHLGSGFAEDGMAEDITEGSEFDYY KONRSARTLWHDHAMHTAFENAVRGVAGLYMLDPAEDALNPSGGEPIPIILTS KYRANANIVTWTGELNLSFWDGTVHVGQPMPEVNPFRKREFDLAAVSRSGLAF ADTAIDTRLPFKIASDSCLEHPATSLIYSMAERYEVPFSPSYAGKTIELRLN GGSGGGIGTIDIDNTDKVMKFEVADDTTOPDSVVPANLEKDPFSPPTNPQRF GRTPPTWINGVADVQNRLLANVPVGTVEHMLINAGSMWHPHILHVDPEVISR TSGNNARTVMPEYSGLDVWVIGRETVVEAHAPPGVYMFCHNLIEDHDMAAA FNAVVLDPGYGNATVFDVPMELMQARPELGEFQAGSGQSVQAVMERIQTMAYRNP YAAADE"			
CDS				
BASE COUNT	440 a	549 c	436 g	517 t
ORIGIN				
sig.peptide	66..179			
mat.peptide	180..1781			
polya_signal	1832..1837			
polya_site	1942			
Alignment Scores:				
Pred. No.:	1,22e-129			Length: 1942
Score:	1724.50			Matches: 322
Percent Similarity:	74.34%			Conservative: 75
Best Local Similarity:	60.30%			Mismatches: 128
Query Match:	54.08%			Indels: 9

DB: 8 Gaps: 7

US-10-080-233-2 (1-594) x MYRBOR (1-1942)

57 SerProProtyrAsnLeuLeuTyRArgAsnAlaLeuProIleProProValIysGlnPro 76
 192 AGCCACAGATATCCC--ATGTTACAGTACACAGCTGCGCAATTCCTCGTTAAAGAGGCC 248

77 LysMetIleIleThrAsnProValThrGlyLysAspIleTyrTyrGluIleGluIle 96
 249 CGCTTGACTGTAACCAATCTGTGTAATGACAGAGATCTGGTACTATAGAGGTGACAGATC 308

97 LysProPheGlnGlnArgIleTyrProThrIleuArgProAlaThrLeuValGlyTyrAsp 116
 309 AAGCCCTTCACTCAACAGGTTTACCTGATCTGATCCGCTGATCTGGTGGGATATAT 368

117 GlyMetSerProGlyProThrPheAsnValProArgIleThrGluThrValAlaArgPhe 136
 369 GGAATGTCCTCGGCTACTTTCCAGGTTCTCTGAGTGAACAGGTTGCGGCTTC 428

137 IleAsnAsnAlaThrValGluAsnSerValHisLeuHisGlySerProSerArgAlaPro 156
 429 ATTAACAATGCTGAGGCTCTTAAGTCCGTCACCTGACGAGATATCTCTCGTCCGCC 488

157 PheAspGlyTyrAlaGluAspValThrPheProGlyIleTyrLysAspTyrTyrPhePro 176
 489 TTTCAGGATGGGAGAGACATCACGAGCTGCGACCTTCAAGACTATTACTACCCA 548

177 AsnTyrGlnSerAlaArgLeuLeuTyrThrHisAspHisAlaPheMetLysThrAlaGlu 196
 549 AATGACAGTGTGCTCGTACCTATGTCACCAAGTCTGCTATGATATACATCTGCTGAG 608

197 AsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleIleAsnAspGluAlaGluAspAlaLeu 216
 609 AACCCCTACCTGCGCAGGCTGCTCTACATGCTACATGACCCAGCCGAGAGAGCCCTTC 668

217 GlyLeuProSerGlyTyrGlyGluPheAspIleProLeuIleLeuThrAlaLysTyrTyr 236
 669 AACTTGCACAGTGTATGAGGAGTTCATTCCAAGATCTTCAACCTCCACAGCAAAATAT 728

237 AsnAlaAspGlyThrLeuArgSerThrGluGluGluAspGlnAspLeuTyrGlyAspVal 256
 729 ACCGCAACGCGCACTTGTCACCACTATGAGAGCTGAAGCTCACTTGTGGGGATATGA 788

257 IleHisValAsnGlyGlnProTyrPheProPheLeuAsnValGlnProArgLysTyrArgPhe 276
 789 ATTCACGTCGACGAGCAACCTGCGCTTCAAGAAAGCTTGAGCCCTCGCAAAATATGATTC 848

277 ArgPheLeuAsnAlaAlaValSerArgAlaThrPheLeuTyrLeuValAlaArgThrSerSer 296
 849 CGCTTCTCGATGCGCGAGTTTCTGCTCTTTCGCTTCTTCTGCTGATACCTGATCT 908

297 ProAsnValAlaGlyPheProPheGlnValIleAlaSerAspAlaGlyLeuGlnAlaPro 316
 909 ATGACACTGCGCTTCCCTTCAAGTATTTGCTCTCCGATTTCTGCTCTTCTTGAACACCT 968

317 ValGlnThrSerAsnLeuTyrLeuAlaValAlaGluArgTyrGluIleIleAspPhe 336
 969 GCCGATACGACCTGCTGATCATTTCCATGCGCGAGCTTACGAAGTGTGTGACTTTC 1028

337 ThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnVal---AlaGluThrAsnAspVal 355
 1029 TCCGACTATGCTGGCAAGCATTTGAACTTCGCAACCTGCGGCGGTAGCATTTGGCGGCA 1088

356 GlyAspGluAspGlyTyrAlaArgThrLeuGluValMetArgPheValSerSerGly 375
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376 ThrValGlu---AspAsnSerGlnValProSerThrLeuAspAspValProPhePro--- 393
 1149 ACACTAGACGACATCTAGTGTGCTCTGCTACACTTGTGATGTTCCCTCCCTCT 1208

394 ProHisLysGluGlyProAlaAspLysHisPheLysPheGluArgSerAsnGlyHisTyr 413

DB 1209 CCCACACAAACACCCC-----CGAGAGTTCCGCTTGGTCCACCGGTCCTACCTGG 1262

QY 414 LeuIleAsnAspValGlyPheAlaAspValAsnGluThrArgValAlaValProGluLeu 433
 1263 ACTATTATAGTGTGCTTGTGCTGTGATGTTAAACCGTGTGCTTGGCAACCTACCGCTT 1322

QY 434 GlyThrValGluValTyrGluLeuGluAsnSerSerGlyIleTyrPheHisProValHis 453
 1323 GGTACTGTGCGAGCGGTGGAGCTCATCAACCCGCTAAGCGGTGAGACCACTATTCAC 1382

QY 454 IleHisLeuValAspPheLysIleLeuLysArgThrGlyGlyArgGly-----GlnVal 471
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QY 472 MetProTyrGlnSerAlaGlyLeuLysAspValAlaTyrPheGluArgGlyIleThrLeu 491
 1443 ATGCCATACGAGTCC---GGTCTCAAAAGACCTTGTCTGGTGGTCCCGGAAACGTG 1459

QY 492 ThrIleGluAlaHisTyrGlnProTyrPheGlyAlaTyrMetTyrHisCysHisAsnLeu 511
 1500 GTTGTGAGGCTCATATACGCGCTTCCCTGGTGTATGATGATTCATTCATTCGCAAAATTG 1559

QY 512 IleHisGluAspAsnAspMetMetAlaValPheAsnValThrAlaMetGluGluGly 531
 1560 ATTCACGAGATGACAGATATGATGCTGCTTAAAGCCACCGCTGTCGCAATATATGCG 1619

QY 532 TyrLeuGlnGluAspPheGluAspProMetAsnProLysTyrArgAlaValProTyrAsn 551
 1620 TATATGCGACTGTTTTCGTTGACCTATGAGAACAGCTTGGACGCTGCTTATGAA 1679

QY 552 ArgAsnAspPheHisAlaArgAlaGlyLysAsnPheSerAlaGluSerIleThrAlaArgVal 571
 1680 CTCGCGCGCTCAGGCTCAGAGTGCGCAGATTCAGCGTTCAGCTGTATACGAGTAT 1739

QY 572 GlnGluLeuAlaGluGlnGluProTyrAsnArgLeuAspGlu 585
 1740 CAGACTATGCTGAATACAGACTTACCGCCAGCTGACGAG 1781

DB

RESULT 7

E05283

LOCUS E05283 1959 bp RNA linear PAT 29-SEP-1997

DEFINITION Bilirubin oxidase gene.

ACCESSION E05283.1 GI:2173473

VERSION JP 1993199882-A/1.

KEYWORDS Myrothecium verrucaria.

SOURCE Myrothecium verrucaria

ORGANISM Myrothecium verrucaria

REFERENCE 1 (bases 1 to 1959)

AUTHORS Ando, K., Koike, S. and Samejima, T.

TITLE PRODUCTION OF BILIRUBIN OXIDASE

JOURNAL Patent: JP 1993199882-A 1 10-AUG-1993;

AMANO PHARMACEUT CO LTD

OS Myrothecium verrucaria

PN JP 1993199882-A/1

PD 10-AUG-1993

PE 24-JAN-1992 JP 1992034126

PI ANDO KEIICHI, KOIKE, SATOSHI, SAMEJIMA TATSUYA PC

CI2N15/53, CI2N1/19, CI2N9/06, (CI2N15/53, CI2N1.645); CC

strandedness: Double;

CC topology: Linear;

*source: strain-MT-1;

Key Location/Qualifiers

FT CDS 66..1784

FT sig_peptide 66..179

FT mat_peptide 180..1781

FT /product="Bilirubin oxidase".

FEATURES

source 1..1959

/organism="Myrothecium verrucaria"

/db_xref="taxon:5532"

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Pred. No.:	1724.50	Matches:	322	
Score:	74.348	Conservative:	75	
Best Local Similarity:	60.308	Mismatches:	128	
Query Match:	54.088	Indels:	9	
DB:	6	Gaps:	7	
US-10-080-233-2 (1-594) x E05283 (1-1959)				
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DB	132	ACCCACAGATATCCC---ATGTTCACAGTACACACATCCCAATTCCTCTGTAAAGCC	248	
OY	77	LysMetIleIleThrAsnProValThrGlyLysAspIleTyrTyrGluIleGluIle	96	
DB	249	CGCTTGACGTAAACCAATCCTGTGATGACAGAGATGTGCTACTATAGGTCCGATC	308	
OY	97	LysProIleGlnIleArgIleTyrProThrLeuArgProAlaThrLeuValGlyTyrAsp	116	
DB	309	AAGCCCTCCTCACACAGGTTTACCTGACCTTGATCCGCTGATCTGCGGGTATGAT	368	
OY	117	GlyMetSerProGlyProThrPheAsnValProArgGlyThrGluThrValAlaArgPhe	136	
DB	369	GGATGTCTCTCGGCCCTTACTTCCAGGTCTCTGAGGTGAACACATGTGTCCGCTTC	428	
OY	137	IleAsnAsnAlaThrValGluAsnSerValIleLeuHisGlySerProSerArgAlaPro	156	
DB	429	ATTACAAATGCTGAGGCTCTTAACCTCCGTACCTGCACGACGATTCCTCTGCGCCG	488	
OY	157	PheAspGlyTyrAlaGluAspValThrPheProGlyTyrLysAspTyrTyrPhePro	176	
DB	489	TTTGACGATGGGAGAGACATCACCGACCTGCGACGCTCAAGACATTAATACCA	548	
OY	177	AsnTyrGlnSerAlaArgLeuLeuTyrTyrHisAspHisAlaPheMetLysThrAlaGlu	196	
DB	549	AATACACAGTCTGCTGCTACCTATGCTACACGATCATGCTATGCTATCTGCTGAG	608	
OY	197	AsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleIleAsnAspGluAlaGluAspAlaLeu	216	
DB	609	AACGCTACCGTACGACGCTGCTCTCATGCTACACTGACCGACGACGACGCTGTC	668	
OY	217	GlyLeuProSerGlyTyrGlyGluPheAspIleProLeuIleLeuThrAlaLysTyrTyr	236	
DB	669	AACCTGCCAAGTATGCGAGTGCATATTCATATGATCTCAGCGTCCAGACATATAT	728	
OY	237	AsnAlaAspGlyThrLeuArgSerThrGluGlyLysGlnAspLeuTyrPcGlyAspVal	256	
DB	729	ACCCGAACACGCACTTGTGCTACCACTAATGAGACCTCACTATCTGGGGTATGTA	788	
OY	257	IleHisValAsnGlyGlnProTyrProPheLeuAsnValGlnProArgLysTyrArgPhe	276	
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OY	277	ArgPheLeuAsnAlaValSerArgAlaThrPheLeuTyrLeuValAlaArgThrSerSer	296	
DB	849	CGCTTCCTCGATGCCGAGTTTCTGCTTTCGCGCTTACTTTCGCTGATCTGATGCT	908	
OY	297	ProAsnValArgIleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaPro	316	
DB	909	ATCGACACTCGCTTCCCTTCAAGTATATGCTCCGATCTGCGCTTCTTTAAACACCTT	968	
OY	317	ValGlnThrSerAsnLeuTyrLeuAlaValAlaGluArgTyrGluIleIleIleAspPhe	336	
DB	969	GCCGATACACGCTTCTGTATCATATGCGCGAGCGTATGAGAATGTGTGTGACTTC	1028	
OY	337	ThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnVal---AlaGluThrAsnAspVal	355	
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OY	356	GlyAspGluAspGluTyrAlaArgThrLeuGluValMetArgPheValIleSerGly	375	
DB	1089	GGACACATACCGACTATGACACACCGCAAGCTATCGTTTCTGTGTACAGACAC	1148	
OY	376	ThrValGlu---AspAsnSerGlnValProSerThrLeuArgAspValProPhePro---	393	
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OY	394	ProHisLysGluGlyProAlaAspLysHisPheLysPheGluArgSerAsnGlyHisTyr	413	
DB	1209	CCACCCACAAACACCCCC-----CGACAGTTCCGCTTGTGTGCGCACCCGCTCTACCT	1262	
OY	414	LeuIleAsnAspValGlyPheAlaAspValAsnGluArgValIleuAlaLysProGluLeu	433	
DB	1263	ACTATTATGCTGTGCTTCTCTGATGTTCAAAACCGTCTGCTGCAACCTACCCGTT	1322	
OY	434	GlyThrValGluValTyrPcLysLeuAsnSerSerGlyTyrTyrSerHisProValHis	453	
DB	1323	GGTACTGTCGACGTTGGGAGCTCATCAACGCGGTAACGGTTGGACGACACCTATTAC	1382	
OY	454	IleHisLeuValAspPheLysIleLeuLysArgThrGlyValArgGly-----GlnVal	471	
DB	1383	ATCCATCTTGTGACTTCAAGGTGATTTCTGCTACTTCCGCAACACGCGCACAGTC	1442	
OY	472	MetProTyrGluSerAlaGlyLeuLysAspValValTyrPcLysGlyValArgGlyThrLeu	491	
DB	1443	ATGCCATACGATCC---GGTCTCAAGACGTTTCTGCTGCTGCTGCTGCTGCTGCTG	1499	
OY	492	ThrIleGluAlaHisTyrGlnProTyrThrGlyAlaTyrMetTyrHisCysHisAsnLeu	511	
DB	1500	GTTGTGAGGCTCATATACGCGCTTCCCTGGGTATACATGCTTCATGCTCCACATTTG	1559	
OY	512	IleHisGluAspAsnAspMetMetAlaValPheAsnValThrAlaMetLysGly	531	
DB	1560	ATTCAAGAGATCAGATATGATGCTGCTTACGCGCCGCTGCTGCTGCTGCTGCTGCTG	1619	
OY	532	TyrLeuGlnGluAspPheGluAspProMetAsnProLysTyrPcArgAlaValProTyrAsn	551	
DB	1620	TATATGACACGCTTTCCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCG	1679	
OY	552	ArgAsnAspPheHisAlaArgAlaGlyAsnAspSerAlaGluSerIleThrAlaArgVal	571	
DB	1680	CTCGGAGATTCACAGCTCAGAGTGCCAGTTCACAGCTTCAGCTTCAGCTTCAGCTTAT	1739	
OY	572	GlnGluLeuAlaGluGlnLeuProTyrAsnArgLeuAspGlu	585	
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AMU271104				
LOCUS				
DEFINITION				
ACREMONIUM MUTOIRUM mRNA for polyphenol oxidase (ppoA gene).				
ACCESSION				
AJ271104				
VERSION				
AJ271104.1 GI:6996277				
KEYWORDS				
oxidase; ppoA gene.				
SOURCE				
ACREMONIUM MUTOIRUM.				
ORGANISM				
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				
Hypocreales; Hypocreaceae; mitosporic Hypocreaceae; Acremonium.				
REFERENCE				
1 (bases 1 to 2126)				
Gouka,R.J., van der Heiden,M., Swarthoff,T. and Verrips,C.T.				
Cloning of a phenol oxidase gene from Acremonium mutoum and its				
expression in Aspergillus awamori				
Appl. Environ. Microbiol. 67 (6), 2610-2616 (2001)				
JOURNAL				
MEDLINE				
PUBMED				
11375170				
2 (bases 1 to 2126)				
Gouka,R.J.				
REFERENCE				
Submitted (19-JAN-2000) Gouka R.J., Biotechnology, Unilever				
Research Vlaardingen, Olivier van Noortlaan 120, 3133 AT				
Vlaardingen, NETHERLANDS				
JOURNAL				
TITLE				
Direct Submission				
FEATURES				
Location/Qualifiers				

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Alignment Scores:	
Pred. No.:	2.66e-128
Length:	1708.50
Matches:	73.81%
Conservative:	60.07%
Mismatch:	53.57%
Indels:	8
Gaps:	5
DB:	
DS-10-080-233-2 (1-594) x ANU271104 (1-2126)	
57 SerProProGlyAsnLeuTyrArgAsnAlaLeuProIleProProValIysGlnPro 76	
290 AGCCCGGGGACACG--CTGTTCACAGGCGCGGTGCAGATCCCTCCGCAAGAGACCT 346	
77 LysMetIleIleThrAsnProValThGlyLysAspIleTyrTyrGluIleGluIle 96	
347 CTCCTACACCGACCAACCCCTACACAGGTGGGAGATCGACTATGAGATCGAGATC 406	
97 LysProPheGlnIleAspIleTyrProThrLeuArgProAlaThrLeuValGlyTyrAsp 116	
407 AAGCACTTCTCTGACGAGGCTTCTCCGTGACCTGGGCGCTGCTGACCTGTGGGCTACGAC 466	
117 GlyMetSerProGlyProThrPheAsnValProArgGlyThrGluThrValIleArgPhe 136	
467 GGCATCTCCGCCGCTCTACTCTATCATCCAGAGAAGGACGAGACGCTGCTCCGCTTC 526	
137 IleAsnAsnAlaThrValGluAsnSerValIleIleuHisGlySerProSerArgAlaPro 156	

Dd	527	GTGAAACAAGCCACACTGTGAGAGCTCCATCTTCAACGGCTGCTTAAGCCGTGCCCC	586
Qy	157	PhesapglYTPtAlaagLuAspValThrPheProglYtYrLysAspTYrTYrPhePro	176
Dd	587	TGGACGGCTGGGCGTGAAGATGTACCAACCGGGCGATCAAGAGCTACTACTATCCC	646
Qy	177	AsnTYrGlnSerAlaArgLeuLeuTYrTYrHisAspHisAlaPheMetLysThrAlaL	196
Dd	647	AATGGCGAGGGGGGGCGCTTCGTGGGTACCATGACCTGGTATGCATCTGGCCAG	706
Qy	197	AsnAlaTYrPheglYglnAlaGlYAlaTYrIleIleAsnAspGluAlaGluAspAlaLeu	216
Dd	707	AATGGCTACAAAGGCGAGGCTGGGTGGCTACTATCATCCAGACCCCTGGCAGAGATCTTC	766
Qy	217	GlyLeuProSerglYTYrGlyGluPheAspIleProLeuIleLeuThrAlaLysTYrTYr	236
Dd	767	GGTGGCCCGACGGATATGAGAGTACAGACATCCCTCATCTACTACTTCGAAGCAGTAC	826
Qy	237	AsnAlaAspglYThrLeuArgSerThrIuglYglnAspGlnAspLeuTYrPglYAspAl	256
Dd	827	AACCTCGGAGTACTCTTCTCTCCACAAAGGTGAGCAGAGCTCTGGGGAGATGTC	886
Qy	257	IleHisValAsnGlyGlnProTYrProPheLeuAsnValGlnProArgLysTYrArgPhe	276
Dd	887	ATCCAGGTGAACGGAGTCCCGTGGCCCTACTTCGACGTGAGCCAGGAAGTACCGCTTC	946
Qy	277	ArgPheLeuAsnAlaAlaValSerArgAlaPheLeuLeuTYrLeuValArgTYrSerSer	296
Dd	947	CGCCGTCTCGACGCGCGGCTCTCGCTTCCTTCGCTCTACTTTGTTCGACACGGCCAT	1006
Qy	297	ProAsnValArgIleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaPro	316
Dd	1007	GAGGACACCCGCATCCCGTTCAGGTATCCGCTCCGACTCGTGGCTCTGGAGAGCC	1066
Qy	317	ValGlnThrSerAsnLeuTYrLeuAlaValAlaGluArgTYrGluIleIleIleAspPhe	336
Dd	1067	GTCAAGACTTCMAAGCTGTCTCTCCATCTGTGAGCCCTACGAGATATCTCGACTTC	1126
Qy	337	ThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaGluThrAsnAspValGly	356
Dd	1127	TCCGACTTCGAGGGGAAAGACATGAGCTCGGCAACGAGCCGGGGGCGGCTCGGC	1186
Qy	357	AspGluAspGluTYrAlaArgThrLeuGluValMetArgPheValValSerSerGlyThr	376
Dd	1187	ATCGAGGTCACTACAGACGACGACGACAGGTATGCGCTTCAACGTGCGGAGGCCCC	1246
Qy	377	ValGlu-----AspAsnSerGluValProSerThrLeuArgAspValProPheProPro	394
Dd	1247	CTCTCTCTCGCCGACACCTCGTGTGCTCCCTCCATCCCTCGATGAGTGCCTTCCCTCC	1306
Qy	395	HisLysGluGlyProAlaAspLysHisPheLysPheGluArgSerAsnGluHisTYrLeu	414
Dd	1307	AGCACCTGCACACCATGACCATCTCTCCGCTTCGCCGCCACCGCGGCGAGAGGAC	1366
Qy	415	IleAsnAspValGlyPheAlaAspValAsnGluArgValLeuAlaLysProGluLeuGly	434
Dd	1367	ATCAACGGGTTCACCTTCTCCGAGTGGAGAACCCTGCTGGCCACAGTCCCTTGGC	1426
Qy	435	ThrValGluValTYrPglYglnAsnSerSerGlyTYrPheSerHisProValHisIle	454
Dd	1427	ACCGTCCAGCTGTGGCACATGACAAACCGGCGAGGGCTGGACGATCCATTCACATC	1486
Qy	455	HisLeuValAspPheLysIleLeuLysArgThrGlyGly-----Arg	468
Dd	1487	CATCTTGTTGACTTCMAAGATTCGTCTTCGACGGGTGCTACGGGTCTACGACCCGT	1546
Qy	469	GlyGlnValMetProTYrGluSerAlaGlyLeuLysAspValValTYrLeuGlyArgGly	488
Dd	1547	GGT---GTCCGACCGGTAGAGTCTGTGTGTGAAGAGACGTCTGCTACTCTGGCAAGGA	1603
Qy	489	GluThrLeuThrIleGluAlaHisTYrGlnProTYrThrGlyAlaTYrMetTYrHisCys	508

DB 1604 GAGAGGTCGTGCTGAGGCTCAGCTCCTTGCGCGCGCTGACATGTTCCACATGC 1663
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DB 1664 CACAACTCATCCACAGAGCAACAGACATGATGGCGCTTCACATCCCTCCGCC 1723
QY 529 GIUTSGLTYRLEUGLNUASPHENGLUASPPROMETASNPOLYSTRTPARGLAVAL 548
DB 1724 GACTAGGCTACACACTCGAGCGCCCTGACCCCATGACAGACAGATTCGCCGCAAG 1783
QY 549 PROTYRASNARGASNPHEHISALARGALAGLYASNPHESERIALGUSERILETHR 568
DB 1784 CCGTAGCTGACACAGACGCTGAGAGTGGCGAGAACGCTTCAGACACCGACGATCGAG 1843
QY 569 ALAARGVALGINGLUENALAGLUGLNUPTROTYSRASNARGLEUASP---GLUILEU 587
DB 1844 GCGAGGCTCAGCTGATGGCGACCTACCTGACCTACGACACCGGAGCTGGAGATCGTC 1903
588 GIUASPLEUGLYILEGLU 593
1904 TAAAGTCGTGAGCTGAC 1921

RESULT 9
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LOCUS Sequence 1 from patent US 6168936.
DEFINITION ARI22996
ACCESSION ARI22996
VERSION ARI22996.1 GI:14107962
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1958)
AUTHORS Wang, H.
TITLE Phenol oxidizing enzymes
JOURNAL Patent: US 6168936-A 1 02-JAN-2001;
FEATURES Location/Qualifiers
source 1..1958
/organism="unknown"

BASE COUNT 394 a 593 c 490 g 481 t
ORIGIN

Alignment Scores:
Pred. No.: 2,96e-121 length: 1958
Score: 1620.50 Matches: 331
Percent Similarity: 65.898 Conservative: 67
Best Local Similarity: 54.808 Mismatches: 125
Very Match: 50.824 Indels: 83
Gaps: 11

US-10-080-233-2 (1-594) x ARI22996 (1-1958)

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QY 77 Lys-----Met-IleIle 80
DB 202 AAGTAGTAAGTACATTCTATAGCTAGACAGACCAAGCTTGCTATATCATTTGACATCCCT 261
QY 80 ethrAsnProValThnGlyLysAspIleTyrTyrGluIleGluIleLysProPheGlu 100
DB 262 CCCCACCCACACACTGGAGAGACATCTTGTACTACGATGAGATGAGCATTAAGCCCTTCTC 321
QY 100 nGlnArgIleTyRProThrLeuArgProAlaThrLeuValGlyTyRAspGlyMetSerPr 120
DB 322 CCACAGATCTACCTGATCTGAGCGCGCAACATGTTGATACGATGCGCATGCTCC 381
QY 120 oGlyProThrPheAsnValProArgGlyThnGluThnValValAlaArgPheIleAsnAla 140
DB 382 AGGACCTCATCATCGCTTCGTGCGCAAGATGATGTTGCCCTTGTGAACGCGG 441
QY 140 a-----ThrValGIUASNSerValHISLeuHISGLSerProSerArgAlaProPheAs 158

DB 442 AAGAACACCTCTCCACACAGGCTCACCTTGACGGCTCTTCTCTCGAGCTCCCTTTA 501
QY 158 pGlyTrpAlaGluAspValThrPheProGlyGluTyRAspTyRTrpPheProAsnTy 178
DB 502 TGGTGGCTGAGACATACCAAGCTGCGGAGTACAGAGATTAATCTACCCCAACAG 561
QY 178 rGlnSerAlaArgLeuLeuTyrPyrHisAspHisAlaPheMetLysThrAlaGluAsnAl 198
DB 562 GCAGGCTGCCCGCATCTTGTGTACCATACCAATGCCATGTCATCACCGCGAGAACGC 621
QY 198 ATYRPhelGlyGlnAlaGlyAlaTyRILELeAsnAspGluAlaGluAspAlaLeuGlyLe 218
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QY 218 uProSerGlyTyRgLyGluPheAspIleProLeuIleLeuThrAlaLysTyRAsnAl 238
DB 682 CCCACAGGCTACGCGGAGATTGATATCCCTTGTGACTGACCAACGATACAAACGC 741
QY 238 aAspGlyThrLeuArgSerThnGluGluGluAspGlnAspLeuTyrPglAspValIle--- 257
DB 742 AGACGGACTCTCTCTCCACCAATGAGAGATTTCACGCTTCTGGGAGATTAATCA 801
QY 257 ----- 257
DB 802 AGTGTAAATTGAGCCCATTTGAGATGCTTCAATCCTACAAAGATGATGAATTCG 861
QY 258 -----HisValasnGlyGlnProTyRProPheLeuAsnValGlu 270
DB 862 TGCATGCTTAACCAAGTGTATTCACAG -AACGGTAGCCTTGCGCTATGCTCAACGTGCA 920
QY 270 nProArgLysTyRArgPheArgPheLeuAsnAlaAlaValSerArgAlaThrPheLeuTy 290
DB 921 GCGGCGCAAGTACCGCTTCGCTCCCTCAACGCTGCGTCAAGCTTGTGCTGTGA 980
QY 290 rLeuValArgThrSerSerProAsnValArgIleProPheGlnValIleAlaSerAspAl 310
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QY 310 aGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyRLeuAlaValAlaGluArgTy 330
DB 1041 TGGTCTGTGAGGCGCTGTGACACTGACACTGTACATCTATGCTATGCGGAGCGCTG 1100
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DB 1161 TGGTCTGACGCTCTCGGTGTGAGCCTGAGTTGATACACTGACAAAGTATGCGATT 1220
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QY 388 gAspValProPheProPheProHisGlyGlu-----ProAla----- 400
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DB 1329 TGACAGAGATTTACACTTGGCGGCTGCTAAATGACAGTGGACAAATCAACGAGTTACTT 1388
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QY 440 uLeuGluAsnSerSerGlyTyRTrpSerHisProValHisIleHisLeuValAspPheTy 460
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QY 460 sIleLeuLysArgThnGlyLysArgGlyGlnAlaMetProTyRGLuSerAlaGlyLeuTy 480

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GenCore version 5.1.6
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10/2/03
C. H. H.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 3, 2003, 20:55:31 ; Search time 381 seconds

(without alignments)
3510.990 Million cell updates/sec

Title: US-10-080-233-2

Perfect score: 3189

Sequence: 1 MFKSMQLAASGLISVLG.....AQEPEYRNDELLELDGIEE 594

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 segs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008
Listing first 45 summaries

Command line parameters:

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-DB=N.Geneseq_101002 -OFMT=fasta -SUFFIX=ing -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=10
-MODE=LOCAL -OUTFMT=pct -NORM=score -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MAP -LARGEORDER -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3189	100.0	1791	20	AA227601	Stachybotrys pheno
2	3189	100.0	1791	21	AA50019	Stachybotrys chart
3	3189	100.0	1791	21	AA51314	Stachybotrys chart
4	3189	100.0	1791	24	AA47584	S. chartarum phenol
5	3171	99.4	1791	20	AA227602	Stachybotrys pheno
6	3056	95.8	1791	20	AA227603	Stachybotrys pheno
7	3056	95.8	1791	20	AA227604	Stachybotrys pheno
8	3056	95.8	1791	20	AA227605	Stachybotrys pheno
9	3056	95.8	1791	20	AA227606	Stachybotrys pheno
10	3056	95.8	1791	20	AA227607	Stachybotrys pheno
11	3056	95.8	1791	20	AA227608	Stachybotrys pheno
12	3056	95.8	1791	20	AA227609	Stachybotrys pheno
13	3056	95.8	1791	20	AA227610	Stachybotrys pheno
14	1870	58.6	2063	21	AA51315	Stachybotrys pheno
15	1870	58.6	2063	21	AA51316	Stachybotrys pheno
16	1870	58.6	2063	21	AA51317	Stachybotrys pheno
17	1868	58.6	2063	21	AA51318	Stachybotrys pheno
18	1868	58.6	2063	21	AA51319	Stachybotrys pheno
19	1868	58.6	2063	21	AA51320	Stachybotrys pheno
20	1724.5	54.1	1959	14	AA047790	B. spicifera phenol
21	1708.5	53.6	2110	21	AA61243	DNA encoding a phe
22	1620.5	50.8	1958	22	AA82585	Stachybotrys chart
23	1620.5	50.8	1958	22	AA82586	Stachybotrys chart
24	1620.5	50.8	1958	22	AA82587	Stachybotrys chart
25	1620.5	50.8	1958	22	AA82588	Stachybotrys chart
26	1620.5	50.8	1958	22	AA82589	Stachybotrys chart
27	1620.5	50.8	1958	22	AA82590	Stachybotrys chart
28	1620.5	50.8	1958	22	AA82591	Stachybotrys chart
29	1620.5	50.8	1958	22	AA82592	Stachybotrys chart
30	666.5	20.9	858	21	AA50022	Stachybotrys chart
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33	666.5	20.9	858	21	AA50025	Stachybotrys chart
34	588	18.4	109319	22	AA50893	Stachybotrys chart
35	516.5	16.2	3446	23	AA65057	Stachybotrys chart
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37	500	15.7	1533	22	AA66019	Stachybotrys chart
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39	480.5	15.1	1434	22	AA66021	Stachybotrys chart
40	472	14.8	2014	21	AA647954	Stachybotrys chart
41	409.5	12.8	969	21	AA690646	Stachybotrys chart
42	365.5	11.5	3800	22	AAH54957	Stachybotrys chart
43	363.5	11.4	1230	22	AAH53932	Stachybotrys chart
44	363.5	11.4	3818	22	AAH54003	Stachybotrys chart
45	354.5	11.1	3410	22	AAH54141	Stachybotrys chart

ALIGNMENTS

RESULT 1
AA227601
ID AA227601 standard, DNA; 1791 BP.

AC AA227601;
XX
XX
DT 16-DEC-1999 (first entry)
XX
XX
DE Stachybotrys phenol oxidase coding sequence.
XX
XX Phenol oxidase; enzyme; coloured compound; dye transfer prevention;
XX fabric washing; stain bleaching; anti-dye transfer; detergent; ss.
OS Stachybotrys chartarum.
XX
XX
PN WO9949020-A2.
XX
PD 30-SEP-1999.

XX 23-MAR-1999; 99WO-US06327.
XX 24-MAR-1998; 98US-0046965
XX 22-DEC-1998; 98US-0218702
XX 22-MAR-1999; 99US-0273957.
XX (GENV) GENENCOR INT INC.

XX Amory A, Wang H, Phase P, Lambrechts-Rongvaux A, Wang C;
XX WPI: 1999-591086/50.
XX P-PSDB; AAT39992.

XX Novel enzyme for modifying coloured compounds used to prevent
XX dye-transfer
XX Claim 21; Fig 5; 64pp; English.

This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme
of the invention. The invention is used to modify a coloured compound and
prevent dye transfer during fabric washing, or for strain bleaching or
anti-dye transfer. It is useful in the detergent, paper and pulp, textile
and food industries.

Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;

Alignment Scores:

Pred. No.: 3,68e-303 Length: 1791
Score: 3189.00 Matches: 594
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-10-080-233-2 (1-594) x AA27601 (1-1791)

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QY 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValIleThrGlu 40
DB 67 ATCCCGATGAGACACCGGAGCCACCCATTGAGGCTGTGATCCCGAAGTGAAGCTGAG 126
QY 41 ValPheAlaAspSerLeuLeuAlaAlaIleGlyAspAspAspTrpGluSerProTrpTyr 60
DB 127 GTCCTCGCTGACTCCTCTCTGCTGACAGCCGATGACGACTGGGAGTCACTTCATAC 186
QY 61 AsnLeuLeuTyrArgAsnAlaLeuProIleProProValLysGlnProLysMetIleIle 80
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QY 81 ThrAsnProValIleThrGlyLysAspIleTrpTyrTyrGluIleGluIleLysProPheGln 100
DB 247 ACCAACCCTGTCCACCGGAGACATTTGTAATGATGAGATCAGATCAACCATTTAG 306
QY 101 GlnArgIleTyrProThrLeuArgProAlaThrLeuValIleGlyTyrAspGlyMetSerPro 120
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QY 221 GlyTyrGlyGluPheAspIleProLeuIleLeuThrAlaLysTyrTyrAsnAlaAspGly 240
DB 667 GGTATGCGGAGATTCGATATCCCTGATCTCTGACGGCCAGATTAACGCCGATGCT 726
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DB 727 ACCCTGGCTTGACGAGGAGGTGAGACAGCAAGCTGTGGGAGATGTCATCCATGTAAC 786
QY 261 GlyIleProTrpProPheLeuAsnValGlnProArgLysTyrArgPheArgPheLeuAsn 280
DB 787 GGACAGCCATGCGCTTCTTACGTCAGCCCGCAAGTACCGCTTCCGATTCCTCAAC 846
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Oy 341 GYGVInThLeuAspLeuArgAsnValAlaGluThraAsnAspValGlyAspGluAspGlu 360
Db 1027 GGCAGACTCTTGACTGCGCAACCTTGCTGAGACCAACGATGCGGACGAGAGATAG 1086
Oy 361 TyraAlaArgThraLeuGluValMetArgPheValValSerSerGlyThrValGluAspAsn 380
Db 1087 TACGCTGCACCTCTCGAGGTATGCGTTCGTCGACCTCTGGACACTGTTGAGACAC 1146
Oy 381 SerGluValProSerThraLeuArgAspValProPheProOHHisLysGluGlyProAla 400
Db 1147 AGCCAGGTCCTCCACTCTCCGTCGACCTCTTCCCTCCCTCCACAAAGAGGCCCCGCC 1206
Oy 401 AspLysHisPheLysPheGluArgSerAsnGlyHisLysLysLeuIleAspAspValGlyPhe 420
Db 1207 GACAAAGCACTTCAAGTTGAAGGACGACGACACTACGATCAACGATGTTGGCTTT 1266
Oy 421 AlaAspValAsnGluArgValLeuAlaLysProGluLeuGlyThrValGluValTPsGlu 440
Db 1267 GCCGATGTCATGAGCGTCTCTGGCCAAAGCCCGACGCTCGGACCGTTGAGTCTGGAG 1326
Oy 441 LeuGluAsnSerSerGlyGlyTrpSerHisProValHisLysLeuValAspPheLys 460
Db 1327 CTCGAGAACTCTCTGGAGGCTGGAGCCACCCGCTCCACATTCACCTTGTGACTTCAAG 1386
Oy 461 IleLeuLysArgThraGlyArgGlyGluValMetProGlyLysSerAlaGlyLeuLys 480
Db 1387 ATCTCAAGCAACTGCTGCTGCTGCGCCAGGTCATGCTTCACTGCTGCTGCTTAA 1446
Oy 481 AspValValTrpLeuGlyArgGlyGluThraLeuThrIleGluAlaHisLysTrpGluProTrp 500
Db 1447 GATCTCGTCTGTTGGGCGAGGGGTGAGACCTGACCACTGAGGCCCTACCAACCCCTGG 1506
Oy 501 ThrGlyAlaTrpMetTrpHisCysHisAsnLeuIleHisGluAspAsnAspMetAla 520
Db 1507 ACTGAGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1566
Oy 521 ValPheAsnValTrpAlaMetGluGluLysGlyTrpLeuGluGluAspPheGluAspPro 540
Db 1567 GTATTCAACGTCACCGGCGATGAGAGAGAGATATCTTCAGAGGACTTGGAGAGACCC 1626
Oy 541 MetAsnProLysTrpArgAlaValProTrpAsnArgAsnAspPheHisAlaArgAlaGly 560
Db 1627 ATGAACCCCAAGTGGCGCGCTCTTACCAACGCAACGACTTCCATGCTCGCGCTGGA 1686
Oy 561 AsnPheSerAlaGluSerIleThrAlaArgValGluGluLeuAlaGluGluProTrp 580
Db 1687 AACTTCTCCGCGAGTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1746
Oy 581 AsnArgLeuAspGluIleLeuGluAspLeuGlyIleGluGlu 594
Db 1747 AACCGCTCGATGAGATCTCGAGAGATCTTGAATCGAGGAG 1788

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RESULT 3
AA51314 standard; DNA; 1791 BP.

AA51314:
09-OCT-2000 (first entry)
Stachybotrys chartarum phenol oxidizing enzyme cDNA.
Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;
pulp; paper bleaching; ss.
Stachybotrys chartarum.
Key location/Qualifiers
CDS 7..1791
FT /*tag= a

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FT  /product= Phenol_Oxidizing-Enzyme
XX  MO200037654-A2
PN  29-JUN-2000.
PD  20-DEC-1999; 99WO-US31009.
XX  23-DEC-1998; 98US-0220871.
PR  23-JUN-1999; 99US-0338723.
XX  (GENEV) GENENCOR INT INC.
PA  Wang H, Bodie EA.
PI  WPI: 2000-452191/39.
DR  P-PSDB; AA196761.
XX  New phenol oxidizing enzyme for modifying colors associated with dyes
PT  or colored compounds, is obtained from fungus and is encoded by a
PI  nucleic acid comprising a specific nucleotide sequence
XX  Disclosure: Fig 5A-B; 45pp; English.
PS  This cDNA encodes Stachybotrys chartarum phenol oxidizing enzyme.
CC  Phenol oxidizing enzymes encoded by nucleic acid sequences which
CC  hybridize to this DNA are claimed, as long as the enzyme is capable of
CC  modifying the colour associated with dyes or coloured compounds. The
CC  enzymes are useful in detergent compositions and for modifying colors
CC  associated with dyes or colored compounds which occur in stains in a
CC  sample. The enzymes are also useful for pulp and paper bleaching,
CC  anti-dye transfer in detergent and other textile applications.
SQ  Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;

Alignment Scores:
Pred. No.: 3,686-303 Length: 1791
Score: 3189.00 Matches: 594
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-10-080-233-2 (1-594) x AA51314 (1-1791)
Oy 1 MetLeuPheLysSerTrpGluLeuAlaAlaLaserglyLeuSerGlyValLeuGly 20
Db 7 ATGCTGTTCAAGTCAATGCAACTGCGACACCTCCGCGCTCTGCTGAGTCTCTGGC 66
Oy 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40
Db 67 ATCCGATGACACCGCGAGCCACCCCATTTAGGCTGTGATCCCGAAGTGAAAGACTGAG 126
Oy 41 ValPheAlaAspSerIleLeuAlaAlaAlaGlyAspAspTrpGluSerProProTrp 60
Db 127 GTCTTGGTGACTCTCTCTGCTGCAAGAGGCACTGAGGAGTCACTCCCTCATAC 186
Oy 61 AsnLeuLeuTrpArgAsnAlaLeuProIleProProValLysGluProLysMetIle 80
Db 187 AACTGCTTACAGAGATGCCCTGCCAATTCACCTGTCAGACGCCCAAGATATCAT 246
Oy 81 ThrAsnProValThrGlyLysAspIleTrpTrpTrpGluIleGluIleLysProPheGlu 100
Db 247 ACCAACCCTGTCACCGGCAAGAGATTTGATGATGATGATGATGATGATGATGATGAT 306
Oy 101 GluArgIleTrpProThrLeuArgProAlaThrLeuValGlyTrpAspGlyMetSerPro 120
Db 307 CAAAGGATTTACCCCACTTGGCGCTGCACTCTGCTGCTGCTGCTGCTGCTGCTGCT 366
Oy 121 GlyProThrPheAsnValProArgGlyThrGluThrValValArgPheIleAsnAsnAla 140
Db 367 GGTCTTACTTTCATATGTTCCAGAGAGAAAGAGACTGATGATGATGATGATGATGATGCC 426

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QY	141	ThrValGluAsnSerValHisLeuHisGlySerProSerArgAlaProPheAspGlyTrp	160
Db	427	ACCGTGGAAACTGGCTTCATCTGCACGGCTCCCATCGCTGGCCCTTGATGATGGTGG	486
QY	161	AlaGluAspValTrpIlePheProGlyGluIuTrpLysAspTyrTyrPheProAsnTyrGlnSer	180
Db	487	GCTAGAGATGAGACCTTCCTCGGGGAGTACAAGGATTTACTACTTTCCCACTACCAATCC	546
QY	181	AlaArgLeuLeuLeuTrpTyrHisAspHisAlaPheMetLysThrAlaGluAsnAlaTyrPhe	200
Db	547	GCCCGCCCTTCGTGGTACCATGACACACCCCTTTCATGAGACTGGTGAAAGAGCCCACTTT	606
QY	201	GlyGlnAlaGlyAlaTyrLeuIleAsnAspGluAlaGluAsnAspAlaLeuGlyLeuProSer	220
Db	607	GGTACAGCTGGCGCCCTTACATTATACAGACAGGCTGAGATAGCTCTGGCTTCCTTAGT	666
QY	221	GlyTyrGlyGluPheAspIleProLeuIleLeuThrAlaLysTyrTyrAsnAlaAspGly	240
Db	667	GGCTATGGCGAGTTCGATATCCCTGTGATCTCGACGGCCAGTACTATACGGCGATGT	726
QY	241	ThrLeuArgSerTrpIuGlyGluAspGlnAspLeuTrpGlyAspValIleHisValAsn	260
Db	727	ACCTGGCGTTGGACCGAGGAGGAGACAGGACCTGTGGGAGATGTCATCATCTCAAC	786
QY	261	GlyGlnProTrpProPheLeuAsnValGlnProArgLysTyrArgPheArgPheLeuAsn	280
Db	787	GGACAGCCATGGCTTTCCTTAACTGACGACCCGCAAGTACCGTTTCCGATCTCTCAAC	846
QY	281	AlaAlaValSerArgAlaTrpLeuLeuTyrLeuValArgThrSerProAsnValArg	300
Db	847	GCTCGCGTGTCTGGTGGCTCTCTACTCTCGTCAAGACAGCTGCCAAGCTCAGA	906
QY	301	IleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaProValGlnThrSer	320
Db	907	ATTCTCTTCCAACTCAATGCTCTGATGCTGGTCTCTTCAAGCCCGCTGTACAGCTCT	966
QY	321	AsnLeuTyrLeuAlaValAlaGluArgTrpIuIleIleIleAspPheThrAsnPheAla	340
Db	967	AACTCTTACCTTGGCTGGTGGCCGACGCTTACAGATCATTTAGACTTACCAACTTGGCT	1026
QY	341	GlyGlnThrLeuAspLeuArgAsnValAlaGluTrpAsnAspValGlyAspGluAspGlu	360
Db	1027	GGCCAGACTCTTGAACCTGCGCAAGCTTGCTAGAACCAACGATGTGCGCAGAGATGAG	1086
QY	361	TyrAlaArgThrLeuGluValMetArgPheValValSerSerGlyTrpValGluAspAsn	380
Db	1087	TACCTCGCACTTCGAGAGTGATGCGCTTTCGTGTCAGACTCTGGCAGCTGTGAGAGCAAC	1146
QY	381	SerGlnValProSerThrLeuArgAspValProPheProPheHisGlyGlyProAla	400
Db	1147	AGCCAGGTCCTCCACTCTCCGAGACTTCTTCCCTCTCTCCACAAAGAAAGGCCCCCTC	1206
QY	401	AspLysHisPheLysPheGluArgSerAsnGlyHisTyrLeuIleAsnAspValGlyPhe	420
Db	1207	GACAAAGCACTTCAAGTTGAAACGCAGACGACGACACTACCTGATCAACGATGTGGCTTT	1266
QY	421	AlaAspValAsnGluArgValLeuAlaLysProGluLeuGlyTrpValGluValTrpGlu	440
Db	1267	GCCGATGTCATGAGCGTGTCTGCGCAACCCGCGACTCGGCAACCGCTTGAAGTCTGAGAG	1326
QY	441	LeuGluAsnSerSerGlyGlyTrpSerHisProValHisIleHisLeuValAspPheLys	460
Db	1327	CTTCAGAAACTCTCTGAGCGCTGAGACCCACCCGCTCAATTCACCTTGTGACTTCAAG	1386
QY	461	IleLeuLysArgTrpIuGlyArgGlyGlnValMetProTyrGluSerAlaGlyLeuLys	480
Db	1387	ATCTCTCAAGCCAACTGGTGTGTGGGCGAGGTCAAGCTCAAGCTCGATGCTGGCTGTAAAG	1446
QY	481	AspValValTrpLeuGlyArgGlyGlyIuThrLeuThrIleGluAlaHisTyrGlyProTrp	500
Db	1447	GATGTCGTCGTGGTGGGAGGGGAGACCTGTACAACTCAAGAGGCCCACTACCAACCTCGG	1506
QY	501	ThrGlyAlaTyrMetTrpHisCysHisAsnLeuIleHisGluAspAsnAspMetAla	520

Dd	1507	ACTGAGCTTACATGTGGCACTGTGCACAACTCATTCACGAGATAACAGCATATATGGCT	1566
Oy	521	ValPheAsnValTrhAlaMetCgluLysClyTyrrLeuGlnGluAspPheGluAspPro	540
Dd	1567	GTAATTCAACGTCACCAGCCGATCGAGAGAGAAGGATATCTTCAGGAGAGACTTGAGAGACCCC	1626
Oy	541	MetsAnPrPolYstTPHtgaIvalAProTYrAsnArgAsnAspPheHisAlaArgAlaGly	560
Dd	1627	ATGAACCCCAAGTAGTGCGGCCGCTTCATCAACCGCAACGCACTTCATAGCTCGCGCTGGA	1686
Oy	561	AsnPheSerAlaGluSerIleThrAlaArgValGlnGluLeuAlaGluGlnGluProTYr	580
Dd	1667	AACCTTTCGCCGAGTCCATACATGCCCCGAGATGCCAGAGAGCTGCGCGAGACGACCGATAC	1746
Oy	581	AsnArgLeuAspGluIleLeuGluAspLeuGlyIleGluGln	594
Dd	1747	AACCGCCTCGATGAGATCTCGAGAGATCTTGGAATCGAGAG	1788
RESULT 4			
AL47584	ID	AA47584 standard; cDNA; 1791 BP.	
XX	AA47584;		
XX	AA47584;		
Dt	13-SEP-2002	(first entry)	
Dx	S chartarum phenol oxidizing enzyme cDNA.		
Dx	Phenol oxidizing enzyme; enzyme; fungus; redox reaction; detergent;		
KW	paper industry; pulp industry; textile; food industry; gene; ss.		
OS	Stachybotrys chartarum.		
Key	Location/Qualifiers		
FT	CDS	7..1791	
FT	/tag=	a	
FT	/product=	"phenol oxidizing enzyme"	
PN	US6399329-B1.		
PD	04-JUN-2002.		
XX	21-DEC-1999;	99US-0468578.	
XX	12-DEC-1998;	99US-Q220871.	
PR	23-JUN-1999;	99US-0338723.	
PA	(GENV) GENENCOR INT INC.		
XX	Wang H, Bodie EA;		
PI	WI: 2002-498835/53.		
DR	P-PDB: AAO18210.		
PT	New polynucleotides encoding phenol oxidizing enzymes, useful for		
PT	preventing the transfer of dyes in solution from one textile to another		
PT	during detergent washing -		
PS	Disclosure: Fig 5; 37pp: English.		
XX	The present invention provides the protein and coding sequences of phenol		
CC	oxidizing enzymes from Stachybotrys chartarum, Bipolaris spicifera and		
CC	Curvularia pallescens. These enzymes are useful in the textiles, paper,		
CC	pulp, detergent and food industries. In particular they are useful for		
CC	preventing the transfer of dyes in solution from one textile to another		
CC	during detergent washing (dye transfer inhibition). The present sequence		
CC	is the S. chartarum phenol oxidizing enzyme cDNA.		
XX	Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;		
SO	Alignment Scores:		
	3.68e-303	Length:	1791
	Pred. No.:		

Score: 3189.00 Matches: 594
 Percent Similarity: 100.00% Conservatave: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-10-080-233-2 (1-594) x AAL47584 (1-1791)

QY 1 MetLeuPheLysSerTrpGlnLeuAlaAlaSerGlyLeuLeuSerGlyValLeuGly 20
 DB 7 ATGCTGTTCAAGTATGAGCACTGCGACAGCACTCCGGGCTCCTGCTGGAGTCTCGGC 66
 QY 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40
 DB 67 ATCCGATGGACACCGGACGCCACCCCATGTAGGCTGTGATCCGAGTGAAGACTGAG 126
 QY 41 ValPheAlaAspSerLeuLeuAlaAlaValAspAspAspTrpGluSerProProtyr 60
 DB 127 GTCTTCGCTGACCTCTCTCTGTCGACAGCGAGTACGACTGGAGTCACTCCATAC 186
 QY 61 AsnLeuLeuTyArgAsnAlaLeuProIleProProValLysGlnProLysMetIleIle 80
 DB 187 AACCTGCTTACAGGAATGCGCTGCAATTCACCTGTCAGACAGCCCAAGATGATCAT 246
 QY 81 ThrAsnProValIleThrGlyLysAspIleTrpTyrgluIleGluIleLysProPheGln 100
 DB 247 ACCAACCTGTGCACCGGACAGACATTTGTACTATGATGAGATCAGATCAACCATTCAG 306
 QY 101 GlnArgIleTyProThrLeuArgProAlaThrLeuValGlyTyArgAspLysMetSerPro 120
 DB 307 CAAGGATTTACCCACCTTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366
 QY 121 GlyProThrPheAsnValProArgGlyThrGluThrValValArgPheIleAsnAla 140
 DB 367 GGTCTCTCTTCAATGTTCCAGAGAACAGACTGATGAGTTGATGATGATGATGATGATG 426
 QY 141 ThrValGluAsnSerValHisLeuHisGlySerProSerArgAlaProPheAspGlyTrp 160
 DB 427 ACCGTGAGAACCTGGTCCATCTGACGCTCCCATCGCTGCTGCTGCTGCTGCTGCTGCT 486
 QY 161 AlaGluAspValIleThrPheProGlyIleTyrglyLysAspTyrglyPheProAsnTyrglnSer 180
 DB 487 GCTAAAGATGTGACCTTCCCTGGGAGTACAAAGATTACTTCTTCCCACTTACCAATCC 546
 QY 181 AlaArgLeuLeuTyrglyHisAspHisAlaPheMetLysThrAlaGluAsnAlaTyrglyPhe 200
 DB 547 GCCCGCTCTGTGTGACATGACAGCACGCTTCAATGAAGACTGTGAAGATGCTTACTTT 606
 QY 201 GlyGlnAlaGlyAlaTyrglyIleIleAsnAspGluAlaGluAspAlaLeuGlyLeuProSer 220
 DB 607 GGTGAGGCTGGCGCTCAATTATACGACGAGGCTGAGATGCTTCCGCTTCCAT 666
 QY 221 GlyTyrglyGluPheAspIleProLeuIleLeuThrAlaLysTyrglyTyrglyAsnAlaAspGly 240
 DB 667 GGTATGGCGAGTTCGATATCCCTGTGATCTGAGCGCAAGTACTATTAAGCCGAGTGT 726
 QY 241 ThrLeuArgSerThrGlnGlyGluAspGlnAspLeuTrpGlyAspValIleHisValAsn 260
 DB 727 ACCGTGCTTGCAGCGAGGTGAGACAGCACTGTGGGAGATGTCATCAGTCAAC 786
 QY 261 GlyGlnProTrpProPheLeuAsnValGlnProArgLysTyrglyArgPheArgPheLeuAsn 280
 DB 787 GGAAGCGCATGGCTTTCCTTAACGTCCAGCCGCAAGTCCCTTTCGATTCCTCAAC 846
 QY 281 AlaAlaValSerArgAlaTrpLeuLeuTyrglyLeuValArgThrSerSerProAsnValArg 300
 DB 847 GCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
 QY 301 IleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaProValGlnThrSer 320
 DB 907 ATTGCTTCCAAAGCATGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
 QY 321 AsnLeuTyrglyLeuAlaValAlaGluArgTyrglyIleIleIleAspPheThrAsnPheAla 340

DB 967 AACCTTACCTTGTGCTTGGCCGACGCTTACAGAGATCATTTATGACTTCCACCACTTGTCT 1026
 QY 341 GlyGlnPheLeuAspLeuArgAsnValAlaGluThrAsnAspValGlyAspGluAspGlu 360
 DB 1027 GGCAGACTCTTGCACCTGCGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1086
 QY 361 TyrAlaArgThrLeuGluValMetArgPheValValSerSerGlyThrValGluAspAsn 380
 DB 1087 TACGCTGCACCTTCGAGAGTATGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1146
 QY 381 SerGlnValProSerThrLeuArgAspValProPheProPheProHisLysGlyProAla 400
 DB 1147 AGCCAGGTCCCTCCACTCTGCTGAGCTTCTTCCCTCCCTCAAGAAAGGCCGCC 1206
 QY 401 AspLysHisPheLysPheGluArgSerAsnGlyIleIleIleIleAsnAspValGlyPhe 420
 DB 1207 GACAAAGCACTTCAAGTTTGAAGCGAACGACGACACTACCTGATCAACGATGTGGCTTT 1286
 QY 421 AlaAspValAsnGluArgValLeuAlaLysProGluLeuGlyThrValGluValTrpGlu 440
 DB 1267 GCCATGTGATGAGCGGTGCTGCTGCGCAAGCCGAGCTCGGACCGTTGAGGTGGGAG 1326
 QY 441 LeuGluAsnSerSerGlyGlyTrpSerHisProValHisIleHisLeuValAspPheLys 460
 DB 1327 CTCGAGAACTCTCTGGAGGCTGAGGCCACCCCTCCACATTCACCTTGTGACTTCAAG 1386
 QY 461 IleLeuLysArgThrGlyArgGlyValGlnValMetProTyrglyGluSerAlaGlyLeuLys 480
 DB 1387 ATCTCAAGCCAACTGGTGGTGTGCTGCGCAAGCTATGCTCTGAGTGTGCTGCTGCTTAA 1446
 QY 481 AspValValTrpLeuGlyArgGlyGluThrLeuThrIleGluAlaHisTyrglnProTrp 500
 DB 1447 GATGTGCTGTGTTGGGAGGGGTGAGACCTTGACATTCGAGGCCCACTTACCAACCTGG 1506
 QY 501 ThrGlyAlaTyrglyMetThrHisCysHisAsnLeuIleHisGluAspAsnAspMetIleAla 520
 DB 1507 ACTGAGCTTACATGTGACCTGTACAACTCTCAATCAAGGATGATGATGATGATGATG 1566
 QY 521 ValPheAsnValIleThrAlaMetGluGluLysGlyTyrglyLeuGlnGluAspPheGluAspPro 540
 DB 1567 GTATTCAACGCTACCGCCATGAGAGAGAGAGATATCTTCAGAGACTTGGAGACCCC 1626
 QY 541 MetAsnProLysTrpArgAlaValProTyrglyAsnArgAsnAspPheHisAlaArgAlaGly 560
 DB 1627 ATGAACCCCAAGTGGGCGGCTTCTTACAAACGCAACGACTTCCATGCTCGCGCTGGA 1686
 QY 561 AsnPheSerAlaGluSerIleThrAlaArgValGlnGluLeuAlaGluGlnGluProTyrgly 580
 DB 1687 AACTTCTCCCGCGAGTCCATCTGAGCCGAGTGTGAGAGCTGTGCGGACGACGACGCTTAC 1746
 QY 581 AsnArgLeuAspGluIleLeuGluAspLeuGlyIleGluGln 594
 DB 1747 AACCGCTCGATGATCTTGGAGGATCTTGAATCCAGAGAG 1788

RESULT 5
 ID ABA92911 standard; DNA; 7248 BP.
 AC ABA92911:
 DT 09-APR-2002 (first entry)
 DE Stachybotrys chartarum laccase gene.
 DX Stachybotrys chartarum laccase.
 KW laccase; enzyme; blue copper oxidase; fungal; oxidation; reduction;
 KM copper; metal cofactor; gene; plant; ds.
 OS Stachybotrys chartarum.
 XX WO200196543-A2.
 PN 20-DEC-2001.
 PD

OY	341	GLYGLNHRILEUAPRIEAPRGASVVALAIGELNHRISNAPRVALIGYASPCILNAPGILU	360
Db	1027	GGCCAGACCTCTTGACCTCGCCACAGCTTGCTAGACCAACGATGTCGGCGAGAGATAG	1086
OY	361	TYRALAATGTHRLAUGLVALMetARPhEVALSerSerGIYthValGIuAPRsn	380
Db	1087	TAGCCTGGCACTCTCGAGGTGATGCGCTCTGCTGACGTCTGGCACCTGTGAGACAAAC	1146
OY	381	SERGLNVALProSerTHRLAUARGASPRVALProPheProPRONISLYSGILYPRCALA	400
Db	1147	AGCCAGGTCCCTCCACTCTCCGTAGAGTTCTTCCCTCTCCATCAAGAGAGCCCCC	1206
OY	401	ASPRYSNHPheLYSPhneGIUARGSerASNLYHISTYTLLEUThEASNAPVALGIYPhE	420
Db	1207	GACACGACCTTCAGATTGAACGCGACCAACGCACTACTCGATTCACAGATGTGGCTTT	1266
OY	421	ALAAPRVALASngILUARGVALLEUALALysProGILUENGILYthVALIGLVALTPGLU	440
Db	1267	GGCGATGTCATGAGCGGTCTCTGCGCCAGGCCGACCTCGGCACCGTTGAGGTCTGGAG	1326
OY	441	LEUGILUASNserSerGIYGLYTPSerHISProVALHISILENISLEUVALASPPhELYS	460
Db	1327	CTCCAGAACTCCTCTGGAGCGCTGGAGGCCACCCCGTCCACATTCACCTGTGGACTTCAAG	1386
OY	461	ILELEULYSARGTHNGILYGLYARGGLYGLNVALMetProTYTGILUSerHISAGLYLEULYS	480
Db	1387	ATCTCTCAAGCAACTGGGTGGTGTGGCCAGGATCAAGCTCAAGCATGCTGGCTGTAAAG	1446
OY	481	ASPRVALTPLEUGILYARGGLYGLUThRLAUthRLIEGILUALHISTYGLNProTHP	500
Db	1447	GATTCGTCTGTGGTGGCGAGGGGTGAGAACCTTGACATPCAGAGGCCACTACCAACCTTGG	1506
OY	501	THRGILUALTYMetTRPHISCYuSNISASNLEUThENISGLUASNAPRsnMetMetALA	520
Db	1507	ACTGGACCTTACAAGTGGCACTGTCCAAACCTCACTTACAGSAGATTAACGATGATGCTT	1566
OY	521	VALPheASNVALThRLAMetGILNGLYGLYTYTLLEUGILNGLUshARPhGILUAPRO	540
Db	1567	GTATTCAAAGCACCGGCATGGAGAGAGAGGATATCTCAAGAGCACTTGSAGAGACCCC	1626
OY	541	METASNProLYSTPRARGALAVAlProTYASNATrgASNAPRsnHISALARGALAGLY	560
Db	1627	ATGAACCCCAAGTGGCGGCGCTTCCTTAACAACCCCAAGCATCTGCATGCTGGGCTGGA	1686
OY	561	ASNPhESerHISAGLUSerHIEthRLALARGVALINGLULeUALAGLUGLNGILNProTYT	580
Db	1687	AACCTTCTCGCGGAGTCCATCACTACAGCCCGAGACTCGAGAGCTGGCCGAGACAGACCTGAC	1746
OY	581	ASNARGLEUASNPGILILEUGILUASNPRLEUGILYILEUGILU 594	
Db	1747	AACCGCCTCGATGAGATCTCTGGACATCTCTGTGAATCAGAGAG 1788	

RESULT 7	
AA225735	
ID	AA25735 standard; DNA; 2067 BP.
XX	
XX	AA225735;
AC	
DT	05-JAN-2000 (first entry)
XX	
DE	Stachybotrys chartarum phenol oxidising enzyme PCR fragment.
XX	
KM	Stachybotrys chartarum: phenol oxidising enzyme: colour; dye;
KM	detergent; anti-dye transfer; stain removal; bleaching; PCR primer; ss.
XX	
OS	Synthetic.
OS	Stachybotrys chartarum.
XX	
PN	MO9949010-A2.
XX	
PD	30-SEP-1999.
XX	

[illegible]

QY 129 YTHGILUTHRALVALAARGPHEILEASNAALATHRYVALGLUASNSERVALHISLEUHI 149
 DB 550 AACAGAGACGTAGTAGTTCATCAACAAATGCCACCGTGAGAACTGGTCCATCTGCA 609
 QY 149 SGYLSERPROSERATGALAPROPHASPGLYTPRALAGLUASPVALLTRPHEPROGLYL 169
 DB 610 CGGCTCCCATCGGCGTCCCTTCGATGGTGGCTGAAATGGACCTTCCCTGGCGGA 669
 QY 169 UTYLYSAPTYTYTPRPHROASNTRYGLINSEALATRYLEULEUTPTYRTHASPHI 189
 DB 670 GTACAGAGATACACTTCTCCCACTACCAATCCGCCCTCTCTGTGTACATGACCA 729
 QY 189 SAlAPHEMELYS----- 193
 DB 730 CGCTTCATGAA-GGATGCTACGAGCCTTATCTTCTGGCTACCTTGGCTAACCA 788
 QY 194 -----THRALAGLUASNALATYTPRHEGLYINLAGLYALATYRILEILAS 209
 DB 789 CTTCCTTTCGTAAGCTGTGAGAAATGCTTCTGTCAGGCTGGCGCTCATATATCA 848
 QY 209 NASPGLUALAGLUASPALALAEUGLYLEUPROSERGLTYRGLYGLUPHEASPILEPROLE 229
 DB 849 CGAGAGGCTGAGGATGCTCCGCTCTCTAGTGGCTATGGCGAGTTCGATATCCCTCT 908
 QY 229 UILELEUTHRALALYSTYTYRASNALASPGLYTHRLEUARGSERTHRGLUGLYLUAS 249
 DB 909 GATCCTGAGCGCCAAAGTACTATAACGCCGATGGTACCTGCGTTCGACCGAGGAGGA 968
 QY 249 PGLIASPLEUTRPGLYASPVALLIETHISVALASNGLYINPROTRPPROPHLEASNYA 269
 DB 969 CCAGAGACCTGTGGGAGATGTCATCCATGTCACGAGACGACATGGCTTTCCTTAACGT 1028
 QY 269 IGLINPROAGLYSTYRARGPHEARGPHELEUASNALALALVALSERATGALATRPLEULE 289
 DB 1029 CCAGCCCGGCAAGTACCTTCCGATTCCTCAAGCTCCGCTGTCTGCTGGCTCTCT 1088
 QY 289 UTYRLEUVALARGTHRSESRPROASNVALARGILEPROPHGLVALILEALASERAS 309
 DB 1089 CTACCTCGTCAGGACACACTCTCCCAAGTCAGATTCCTTCCAAAGTCATTCGCTCGA 1148
 QY 309 PALAGLYLEULEUGLINALAPROVALGINTHRSERASLEUTRYLEUALVALALAGLUAR 329
 DB 1149 TGTGGTCTCTCTCAAGCCCGCTTCACAGCTTAACCTTCCTGTGTGGCGAGCG 1208
 QY 329 GTYRGLULEILELE----- 334
 DB 1209 TTACGAGATCATTTTGTGTATGCCCTCCCTCTCAGCAATGATCAGAACTCTTAAGCT 1268
 QY 335 -----ASPHERTHRASNPHLEALAGLYGLINTHRLASPLEUARASVALALAGL 351
 DB 1269 AACACTTGTAGACTTACCAACTTGTGGCCAGACTCTTGACCTGCGCAACGTTGCTGA 1328
 QY 351 UTHRASNAPVALAGLYASPGLUASPGIUTYRALARGTHRLEUGLVALIMETLAGPHRYA 371
 DB 1329 GACCAAGAGATGTCGGCGAGAGATGATACGCTCGACTCTCAAGGAGGATGCCCTTCTGT 1388
 QY 371 IVALSERSEGLYTHRYVALGLUASPASNSERGLINVALPROSETRHRLAUARGASPVALLPR 391
 DB 1389 CGTCAGCTGTGGCACTGTGAGAACACAGCCAGGTCCCTCCACTCTCCCTGACGTTCC 1448
 QY 391 OPHERPROHISTYLSGLUGLYPTROALASRPLYSHPHELYSPHEGLUARSGERASNGI 411
 DB 1449 TTTCCCTCTCTACAAAGGAGGCCGCCGCAACAGCACTTCAAGTTTGAAACACAGCAACGG 1508
 QY 411 YHISTYRLEULEASNSAPVALAGLYPHEALASPVALLASNGLUARGVALLEUALALYSPT 431
 DB 1509 ACACCTACCTGATCAACAGATGTTGGCTTGGCTGATCAATAGGCTGCGCCAGGCC 1568
 QY 431 OGLILEUGLYTHRYVALGLUVALTRPGLULEUGLUASNSERSEGLYGLYTPRSEHISPT 451
 DB 1569 CGAGCTGGCACCTTGAAGTCTTGAGACTCGAATACTCTCTGAGGCTGGACCCACGCC 1628

QY 451 OVALHISILHISLEUVALASPHLELYSILEULEYLSARGTHRGLYLARGLYGLINVA 471
 DB 1629 CGTCCACATTCACCTGTTGACTTCAAGATCTCAAGGAGACTGGTGGTGGCCAGGT 1688
 QY 471 IMETPROTYRGLINUSERALAGLYLEULYASPVALLTRPLEUGLYARGGLYGLUTHLE 491
 DB 1689 CATGCCCTACAGACTGTGCTGCTTAAGATGTGCTGGTGGGACAGGGGTGAGACCT 1748
 QY 491 UTHRILEGLUALHISTYRGLINPROTPRTHRYVALATYRMEPTRPHISCYSHISASNI 511
 DB 1749 GACCATGAGGCCCACTACCAACCTTGAGACTGAGACTTACATGTGGCACTTCACAACT 1808
 QY 511 UILEHISGLUASPASNSAPMETLALVALPHEASNYALTRALMETGLUGLYSGI 531
 DB 1809 CATTCACAGAGATTAACGACATGATGGCTGTATCAAGCTACCGCCATGAGAGAAAGG 1868
 QY 531 YTYRLEUGLNUASPHREGIUAAPPROMETASNPOLYSTTRPRALVALPROTYRAS 551
 DB 1869 ATATCTTCAGAGAGCTTCGAGAACCCCATGAACCCCAAGTGGCGCGCTTCTTACAA 1928
 QY 551 NARGASNPHEHISALARGALAGLYASNPHESERLAGLUSERILERTHRLAARGVA 571
 DB 1929 CCGCAGACACTTCCATGCTCGCGCTGGAATCTCCGCGAGTCCACTGCGCGAGT 1988
 QY 571 IGLINGLUENALAGLUGLNUPTROTYRASNARGLEUASPGIULEUGLUASPLEUGI 591
 DB 1989 GCAGAGCTGGCCGAGCAGAGCCGTACAAACCGCTCGATGATCTCGAGAGATCTTG 2048
 QY 591 YILEGLUGLU 594
 DB 2049 AATCGAGGAG 2058

RESULT 8

AA227609

ID AA227609 standard; DNA; 2067 BP.

AA227609;

16-DEC-1999 (first entry)

Stachybotrys phenol oxidase coding sequence.

phenol oxidase; enzyme; coloured compound; dye transfer prevention;
 fabric washing; stain bleaching; anti-dye transfer; detergent; ss.

Stachybotrys chartarum.

W09949020-A2.

30-SEP-1999.

23-MAR-1999; 99WO-US06327.

24-MAR-1998; 98US-0046969.

22-DEC-1998; 98US-0218702.

22-MAR-1999; 99US-0273957.

(GENV) GENENKOR INT INC.

Amory A, Wang H, Dhase P, Lambrechts-Rongvaux A, Wang C;

WPI; 1999-591088/50.

Novel enzyme for modifying coloured compounds used to prevent dye-transfer -

Example 17; Fig 9; 64pp; English.

This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme of the invention. The invention is used to modify a coloured compound and prevent dye transfer during fabric washing, or for stain bleaching or anti-dye transfer. It is useful in the detergent, paper and pulp, textile and food industries.

XX Sequence 2067 BP; 445 A; 621 C; 500 G; 501 T; 0 other;
SQ

Alignment Scores:

Pred. No.: 5,17e-290 Length: 2067
Score: 3056.00 Matches: 593
Percent Similarity: 86.70% Conservative: 0
Best Local Similarity: 86.70% Mismatches: 1
Query Match: 95.83% Indels: 91
DB: 20 Gaps: 5

US-10-080-233-2 (1-594) x AA227609 (1-2067)

QY 1 MetLeuPheLysSerTrpGlnLeuAlaAlaSerGlyLeuSerGlyValLeuGly 20
DB 10 ATGCTTTAAAGTCAAGGACGACTGGACGACGCTCCGGGCTCTGTGGAGTCCCTGGC 69
21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40
70 ATCCGATGGACACCGGACGCCACCCATTGAGGCTGTGATCCGAAAGTGAAGACTGAG 129
QY 41 ValPheAlaAspSerLeuLeuAlaAlaGlyAspAspAspTrpGluSerProProTy 60
DB 130 GCTTCGCTGACTCCCTCTCTGTCGACGAGGCGATGAGACTGGAGATCACCCTCATAC 189
61 AsnLeuLeu-----Tyr 64
190 AACTTCCTTTACAGGAGGAGACACCTGTCCACCTGTTTCCCGATAACTAACTCTTAT 249
QY 65 ArgAsnAlaLeuProIleProValLysGlnProLysMet----- 78
DB 250 AGGAATGCCCCCTGCAATTCACCTGTCAGACAGCCCAAGATGATGCTTTGATTTCTCA 309
79 -----IleIleThrAspProValThrGly 87
310 CGAAGCACTCGGCCCGACATAATGTAATCTAGAGATCAATTAACCAACCTGTACCGCAA 369
QY 87 sAspIleTrpTyTrGluIleGluIleLysProPheGlnGlnArg----- 102
DB 370 GGCACATTTGCTACTATGAGATGAGATCAAGCATTTTCAGCAAAAGGTGAGTTGCTCAG 429
103 -----IleTyrProThrLeuArgPr 109
430 AAACCTTGTGTAATTAATCATTTGTTACTGACCTTTCAGATTTCACCCACCTTGGCGCC 489
QY 109 oAlaThrLeuValGlyTyrAspLysMetSerProGlyProThrPheAsnValProArgG 129
490 TGCACACTCTGTCGGCTAGAGATGAGAGCCCTGGTCTTAATGTTCCAGAGG 549
129 yThrGluThrValAlaArgPheIleAsnAsnAlaThrValGluAsnSerValHisLeuH 149
550 AACAGAGACTGATAGTTAGTTCAATCAACATGCGACCGGAGAACTCGGTCATTCGCA 609
QY 149 sGlySerProSerArgAlaProPheAspGlyTyrPalagluAspValThrPheProGly 169
DB 610 CGGCTCCCATGCGCGGCCCTTTCGATGGTGGCGTGAAGATGTGACCTTCCCTGGCGCA 669
169 uTyrLysAspTyTrPheProAsnTyTrGlnSerAlaArgLeuLeuTrpTyHisAspH 189
DB 670 GTACAGAGATTAATTAATTTCCCACTCAACAAATCCGCCGCTTGTGTGACATGACCA 729
QY 189 sAlaPheMetLys----- 193
730 CGCTTTCATGAA -GGATGCTACGAGCCTTTATCTTCTTGCTACCTTTGGTAAACAA 788
QY 194 -----ThrAlaGluAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleLeuAs 209
DB 789 CTTCCTTTCGTAAGACTGCTGAGAAATGCTTACTTGGTTCAGGCTGCGGCTACATATCA 848
QY 209 nAspGluAlaGluAspAlaLeuGlyLeuProSerGlyTyrGlyGlnPheAspIleProLe 229
DB 849 CCAAGAGGCTGAGAGATGCTGCTGCTCTTCTTAAGTGGCTAATGGGAGATTGCAATATCCCTCT 908

QY 229 uIleLeuThrAlaLysTyTrTyrAsnAlaAspGlyThrLeuArgSerThrGluGluAs 249
DB 909 GATCTGACGAGCCCAAGTACTATTAACGCCGATGGTATCCCTGCTTCCAGCCAGGGGTAGCA 968
249 pGluAspLeuTrpGlyAspValIleHisValAsnGlyGlnProTyrProPheLeuAsnVa 269
DB 969 CCAGAGACCTGTGGGAGATGTCAATGATCAAGCAAGGACCACTAGGCTTCTCTTAACG 1028
QY 269 LglnProAlaGlyLysTyArgPheArgPheLeuAsnAlaAlaValSerArgAlaTrpLeu 289
DB 1029 CCAGCCCGCAAGTACCGTTCCGATTCCTCAACGCGTGGCTGTCTGCTGCTGCTCTCT 1088
QY 289 uTyrLeuValArgThrSerSerProAsnValAlaGlyIleProPheGlnValIleAlaSerAs 309
DB 1089 CTACCTGCTGAGGACCAAGCTCTCCCAACGTCACAAATTCCTTCCAAAGTCTTCCCTGCA 1148
QY 309 palaglyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGluAr 329
DB 1149 TGCTGGTCTCTCAAGGCCCGCTGACACTTAACTCTTACCTTGTGTCGAGCG 1208
QY 329 gTyrGluIleIleIle----- 334
1209 TTACGAGATCATTAATGATGCTGCTCCCTCTACAGAAATGACTCAAGAACTTAAGACT 1268
QY 335 -----AspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaG 351
DB 1269 AACACTTGTAGACTTCAACCACTTTGTGCTGCGCAAGCTTGTGCTGCA 1328
QY 351 uThrAsnAspValGlyAspGluAspGluTyrAlaArgThrLeuGluValMetArgPheVa 371
DB 1329 GACCAAGATGTGGGAGAGAGATGATGAGCTGCACTGCACTGCAAGATGATGCGTTCGT 1388
QY 371 lValSerSerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspValPr 391
DB 1389 GCTGACCTCTGGGACGTGTGAGGACCAACACCGTCCCTCCACTCTCTGTCAGCTTCC 1448
391 oPheProProHisLysGluGlyProAlaAspLysHisPheLysPheGluArgSerAsnG 411
DB 1449 TTTCCTCTCCCAAGAAAGAGGCCCGCCGCAAGACACTTCAATTTGAACGCAAGCAAG 1508
QY 411 yHisTyTrLeuIleAsnAspValGlyPheAlaAspValAsnGluArgValAlaLysPr 431
DB 1509 ACACCTACCTGATCAAGAGATGTTGCTTGGCGATGCAATGAGACGTTCTGTCGCAAGCC 1568
QY 431 oGluLeuGlyThrValGluValTrpGluLeuGluAsnSerSerGlyTyrPheHisPr 451
DB 1569 CGAGCTCGGACCGTTGAGGCTGAGGAGCTCGAAGACTCTCTGAGAGGCTGGAGCAACC 1628
451 oValHisIleHisLeuValAspPheLysIleLeuLysArgThrGlyTyrArgGlyGlnVa 471
DB 1629 CGTCCACATTCACCTTGTACTTCAAGATCCCTCAAGCAAGACTGGTGGTGGCCAGGT 1688
QY 471 lMetProTyTrGluSerAlaGlyLeuLysAspValValTrpLeuGlyArgGlyGluThrLe 491
DB 1689 CATGCCCTACGATCTGCTGCTGTTAAGATGTCGCTGCTGTTGGGAGGGGTAGAACCT 1748
QY 491 uThrIleGluAlaHisTyTrGlnProThrPheGlyAlaTyrMetTrpHisGlyHisAsnLe 511
DB 1749 GACCACTGAGGGCCCACTACCAACCTGTGAGCTTCAATGTGACAGCTGTACAAACCT 1808
QY 511 uIleHisGluAspAsnAspMetMetAlaValPheAsnValThrAlaMetGluGluLysG 531
DB 1809 CATTCACGAGGAAAGACATGATGCTGATTAATCAACGTACAGCCATGAGAGAGAGAG 1868
QY 531 yTyrTleGluGlnAspPheGluAspProMetAsnProLysTrpArgAlaValProTyTrAs 551
DB 1869 ATATCTTCAGAGAGACTTGCAGAGACCCCAATGAACCCCAAGTGGCGGCGCTTCTTACA 1928
QY 551 nArgAsnAspPheHisAlaArgAlaGlyAsnPheSerAlaGluSerIleThrPheAlaArg 571
DB 1929 CCGCAAGCACTTCCATGCTGCGGCTGGAACCTTCTCGCGGATCCATCACTGCGCGAG 1988
QY 571 lGlnGluLeuAlaGluGlnGluProTyTrAsnArgLeuAspGluIleLeuGluLysPleuG 591

Db 1989 GCAGAGCTGCGCCGAGCAGAGCCGTACACCGCTCGATGAGATCTTG 2048
Oy 591 YLIEGLUGLU 594
Db 2049 AATCGAGGAG 2058

RESULT 9
AA225728 standard; DNA; 3676 BP.
AA225728:
AC AA225728:
XX 05-JAN-2000 (first entry)
XX Stachybotrys chartarum phenol oxidising enzyme genomic DNA.
DE Stachybotrys chartarum phenol oxidising enzyme; colour; dye;
XX Stachybotrys chartarum; phenol oxidising enzyme; colour; dye;
KW detergent; anti-dye transfer; stain removal; bleaching; ds.

Stachybotrys chartarum.
MO9949010-A2.
XX 30-SEP-1999.
XX 23-MAR-1999; 99WO-EP02042.
XX 24-MAR-1998; 98US-0046969.
XX 22-DEC-1998; 98US-0218702.
XX (UNIL) UNILEVER NV.
XX (UNIL) UNILEVER PLC.
XX Convents D, Amory A, Wang H, Dhaese P, Lambrechts-Rongvaux A,
PI Wang C;
XX WPI; 1999-601211/51.
XX P-PSDB; AAY45222.
XX
XX Detergent composition containing phenol oxidase from Stachybotrys, used
XX to bleach stains and prevent dye transfer
XX
XX Example 14; Fig 6; 56pp; English.
XX
XX The present invention describes a detergent composition containing a
XX purified phenol oxidising enzyme derived from Stachybotrys. The present
XX sequence encodes Stachybotrys chartarum phenol oxidising enzyme. The
XX enzyme can be used to modify the colour of dyes and other coloured
XX compounds (e.g. for use in pulp and paper bleaching also for removing
XX stains, e.g. food, tea, blood etc., from fabrics) and for preventing dye
XX transfer during fabric washing.

SQ Sequence 3676 BP; 822 A; 1056 C; 849 G; 948 T; 1 other;

Alignment Scores:
Pred. No.: 1.15e-289 Length: 3676
Score: 3056.00 Matches: 593
Percent Similarity: 86.70% Conservative: 0
Best Local Similarity: 86.70% Mismatches: 1
Query Match: 95.83% Indels: 91
DB: 20 Gaps: 5

US-10-080-233-2 (1-594) x AA225728 (1-3676)

Oy 1 MetteuphetySerrTPGlnleuAlaAlaAlaSerGlyleuSerGlyValleuGly 20
Db 1044 ATGCTGTTCAGTCAATGCAACTGCGACAGCTCCGGGCTCTGTCTGGAGTCTCTCGGC 1103
Oy 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValIleThrGlu 40
Db 1104 ATCCGATGACACCGGACGACCGCCCATTTAGAGCTGTGATCCCGAAGTAAAGACTGAG 1163

Oy 41 ValPheAlaAspSerIleuAlaAlaAlaGlyAspAspThrPgluSerProThr 60
Db 1164 GTCCTCGCTGACTCCCTCTTGTCTGACAGAGCGCATGACGACTGGAGTCACTTCATAC 1223
Oy 61 AsnleuLeu-----Tyr 64
Db 1224 AACTGTCTTACAGGTGAGACACCTGTCACCTGTGTTTCCCTCGATACATACTCTTAT 1283
Oy 65 ArgAsnAlaIleuProIleProProValIleGlnProIleSmet----- 78
Db 1284 AGGAATGCCCTGCCAATTCACACTCTGTCAAGCAGCCCAAGATGATGTTCTTGAATTTCTA 1343
Oy 79 -----IleIleThrAsnProValIleGly 87
Db 1344 CGAAGCACTCGGCCCGGCTAATGATATTATAGATCATTTACAACTGTCACCGGCA 1403
Oy 87 SASPIleThrPyrIleGluIleGluIleGlyProPheGlnIleArg----- 102
Db 1404 GGACATTTGGTACTATGAGATGAGATCAACCAATTCAGCAAGGCTGAGTTCGTCAG 1463
Oy 103 -----IleTyrProThrIleuArgPr 109
Db 1464 AAACCTTGTTGTAATTAATCATTTGTTACTGACCCCTTTCAGATTTACCCACTTCGCGCC 1523
Oy 109 AlaIleThrIleuValGlyTyrAspGlyMetSerProGlyProThrPheAsnValProArg 129
Db 1524 TGCCACTCTCGCGCTACGATGCGCATGAGCCCTGCTCTTCAATGTTCCAGAG 1583
Oy 129 YThrGluThrValValArgPheIleAsnAsnAlaThrValGluAsnSerValIleIleu 149
Db 1584 AACAGAGACTAGTAGTTCATCAACAAATGCCACGTCGAGAACTGGTCCATCTGCA 1643
Oy 149 SGIYSerProSerArgAlaProPheAspGlyTyrAlaGluAspValThrPheProGly 169
Db 1644 CGGCTCCCATCGCGTCCGCTTTCGATGATGGGTCAAAATGAGACTTCCTCCGCGCA 1703
Oy 169 uTyrIleAspTyrTyrPheProAsnTyrGlnSerAlaArgIleuThrPyrHisAsp 189
Db 1704 GTACAGAGATTACTATCTTCCCACTACCAATCCGCCCTGTGTGTACCATGACCA 1763
Oy 189 sAlaPheMetIlys----- 193
Db 1764 CGCTTTCATGAA--GGTATGCTACAGACCTTATCTTCTTGGCTACCTTGGCTAACCA 1822
Oy 194 -----ThrAlaGluAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleIleAs 209
Db 1823 CTTCCTTTGTAAGACTGTAAGATGCTACTTGGTGAAGCTGGCGCTCAATTAACAA 1882
Oy 209 nasPgluAlaGluAspAlaIleuGlyleuProSerGlyTyrGlyGluPheAspIlePro 229
Db 1883 CGAGGAGCTGAGGATGCTCTCGGCTTCTCTAGTGGCTATGGCGAGTTGATATCCCTCT 1942
Oy 229 uIleIleuThrAlaIleTyrTyrAsnAlaAspGlyTyrIleuArgSerThrGluGluAs 249
Db 1943 GATCCTGACGGCCAGATCTATTAACGCCGATGTATCCCTGCTTCGACCGAGGTTAGGA 2002
Oy 249 pGlnAspIleuThrPgluAspValIleHisValAsnGlyIleProThrProPheIleuAsn 269
Db 2003 CCAGAGCACTGTGGGAGATGTCATCAATGCAAGGACAGCCAGGCTTCCTTAACGT 2062
Oy 269 IGlInProArgIleTyrArgPheArgPheIleuAsnAlaValSerArgAlaIlePleu 289
Db 2063 CCAGCCCGCAAGTACGCTTCCGATTCCTCAACGCTGCCGTGTCTGTGCTGCTCT 2122
Oy 289 uTyrIleuValArgHisSerSerProAsnValArgIleProPheGlnValIleAsnSer 309
Db 2123 CTACCTGCTCAGGACAGCTCTCCCAAGCTAGAAATTCCTTCCAAAGTCAATGCTCTGA 2182
Oy 309 palagIleuIleuGlnAlaProValGlnThrSerAsnIleuTyrIleuAlaValAlaGlu 329
Db 2183 TGCTGTCTCTTCAAGCGCCCGCTTCAGACCTCTTAACCTGTGTGTGCGAGCG 2242
Oy 329 gTyrGluIleIleIle----- 334

GenCore version 5.1.6
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706 is correct

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 3, 2003, 22:57:32 ; Search time 80 Seconds

(without alignments)
2277.075 Million cell updates/sec

Title: US-10-080-233-2

Perfect score: 3189
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Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Delop 6.0, Delext 7.0

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Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-biosum62 -TRANS-human40.cdl
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Database: Issued Patents_NA:*

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6: /cgnt2.6/prodata/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3189	100.0	1791	4	US-09-468-578-5
2	3189	100.0	1791	4	US-09-218-702-1
3	3056	95.8	2067	4	US-09-218-702-5
4	3056	95.8	3677	4	US-09-468-578-1
5	3056	95.8	3677	4	US-09-218-702-3
6	1870	58.6	2063	4	US-09-468-578-6
7	1868	58.6	2905	4	US-09-468-578-3
8	1620.5	50.8	1958	4	US-09-401-476-1
9	1620.5	50.8	2095	4	US-09-401-476-3
10	666.5	20.9	858	4	US-09-468-578-8
11	409.5	12.8	969	4	US-09-134-001C-109
12	200.5	6.3	2249	3	US-08-814-052-19

13	200.5	6.3	2300	3	US-08-814-052-18	Sequence 18, Appl
14	200	6.3	2279	3	US-08-814-052-17	Sequence 17, Appl
15	198.5	6.2	1588	1	US-08-706-037-24	Sequence 24, Appl
16	198.5	6.2	1588	2	US-09-005-397-24	Sequence 24, Appl
17	198.5	6.2	1672	1	US-08-172-331B-13	Sequence 13, Appl
18	187.5	5.9	4403765	4	US-09-103-840A-2	Sequence 2, Appl
19	187.5	5.9	4411529	4	US-09-103-840A-1	Sequence 1, Appl
20	170.5	5.3	1722	4	US-09-221-275-3	Sequence 3, Appl
21	162.5	5.1	1176	3	US-08-669-421-18	Sequence 18, Appl
22	162.5	5.1	1176	4	US-09-389-528-18	Sequence 18, Appl
23	162.5	5.1	1176	4	US-08-181-827A-18	Sequence 18, Appl
24	162	5.1	3183	2	US-08-939-218A-1	Sequence 1, Appl
25	162	5.1	3192	1	US-08-940-661A-1	Sequence 1, Appl
26	162	5.1	3192	2	US-09-083-485-1	Sequence 1, Appl
27	157	4.9	2476	1	US-08-749-882A-1	Sequence 1, Appl
28	157	4.9	2476	2	US-08-539-134-1	Sequence 1, Appl
29	156.5	4.9	3192	1	US-08-706-037-26	Sequence 26, Appl
30	156.5	4.9	3192	2	US-09-005-397-26	Sequence 26, Appl
31	152	4.8	2476	5	PCT-US95-06816-1	Sequence 1, Appl
32	151.5	4.8	3187	5	PCT-US95-06815-1	Sequence 1, Appl
33	149.5	4.7	1170	3	US-08-689-421-20	Sequence 20, Appl
34	149.5	4.7	1170	4	US-09-389-528-20	Sequence 20, Appl
35	149.5	4.7	1170	4	US-08-181-827A-20	Sequence 20, Appl
36	132	4.1	1320	4	US-09-615-192A-207	Sequence 207, App
37	123.5	3.9	534	4	US-09-615-192A-254	Sequence 254, App
38	122.5	3.8	980	4	US-09-615-192A-208	Sequence 208, App
39	121.5	3.8	1161	3	US-08-689-421-22	Sequence 22, Appl
40	121.5	3.8	1161	4	US-09-389-528-22	Sequence 22, Appl
41	121.5	3.8	1161	4	US-09-181-827A-22	Sequence 22, Appl
42	121	3.8	2418	1	US-08-462-84-1	Sequence 1, Appl
43	121	3.8	2418	1	US-08-441-147-1	Sequence 1, Appl
44	121	3.8	2418	5	PCT-US95-07536-1	Sequence 1, Appl
45	113.5	3.6	538	4	US-09-615-192A-118	Sequence 118, App

ALIGNMENTS

RESULT 1
US-09-468-578-5
Sequence 5, Application US/09468578
Patent No. 639329
GENERAL INFORMATION:
APPLICANT: Wang, Huaming
APPLICANT: Bodie, Elizabeth A.
TITLE OF INVENTION: Phenol Oxidizing Enzymes
FILE REFERENCE: GC561-3
CURRENT APPLICATION NUMBER: US/09/468,578
CURRENT FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 09/220,871
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 09/338,723
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1791
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CDNA
US-09-468-578-5

Alignment Scores:
Pred. No.: 0
Score: 3189.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Gaps: 0

US-10-080-233-2 (1-594) x US-09-468-578-5 (1-1791)
OY 1 MetLeuPhelYserTrpGlnLeuAlaAlaSerGlyLeuLeuSerGlyValLeuGly 20

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Db      7 ATGCTGTCAGATCATGCAACTGCGACAGCCCTCGGGCTCTGTCGATGCTCTCGC
QY      21 ILEPROMETASPTThGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40
Db      67 ATCCGAGTACAGACCGGAGCCACCCCAATGAGGTGTGATCCGAAATGTAAGCTAG 126
QY      41 ValPheAlaAspSerLeuLeuAlaAlaIleAspAspSerProGluLysSerProProTy 60
Db      127 GTCCTCGCTGACTCCCTCTGCTGTCAGAGCCGATGAGACGTGGAGTACACTCCATAC 186
QY      61 AsnLeuLeuTyraGlnAlaLeuProIleProProValLysGlnProLysMetIle 80
Db      187 AACTGCTTACAGAAATGCGCTGCAATTCACCTGTCAGACCCCAAGTGTATCAT 246
QY      81 ThrAsnProValThGlyLysAspIleTyrPyrGluIleGluIleLysProheGln 100
Db      247 ACCAACCCCTGTACCGGAGAGACATTTGGTACTATGAGATCGAATCAAGCCATTG 306
QY      101 GlnArgIleTyrProThrLeuArgProAlaThrLeuValGlyTyrAspGlyMetSerPro 120
Db      307 CAAGAGATTATCCCACTGGCCCTGCGCACTCGTGGGTACGATGGCATGAGCCCT 366
QY      121 GlyProThrPheAsnValProArgGlyThrGluThrValValArgPheIleAsnAla 140
Db      367 GGTCTACTTTCAAATGTTCCAGAGAACAGACTGATGATGATGATCATCAACATGCC 426
QY      141 ThrValGluAsnSerValHisLeuHisGlySerProSerArgAlaProPheAspGlyTyr 160
Db      427 ACCCGGAGAACTGGGTCTCATCTGCAAGGCTCCCATGCGCGCTCTTGCATGTGG 486
QY      161 AlaGluAspValThrPheProGlyGluTyrLysAspTyrTyrPheProAsnTyrGlnSer 180
Db      487 GCTGAAGATGTGACCTTCCCTGCGAGTACAAAGATTAATCTTCCCACTACCAATCC 546
QY      181 AlaArgLeuLeuTyrPyrHisAspHisAlaPheMetLysThrAlaGluAsnAlaTyrPhe 200
Db      547 GCCCGCTCTGTGTGATACATGACCACTTTCATGAAGACGCTGAAGATCCCTACTT 606
QY      201 GlyGlnAlaGlyAlaTyrIleIleAsnAspGluAlaGluAspAlaLeuGlyLeuProSer 220
Db      607 GGTGAGCGTGGCGCTTACATTAATCAACAGCAGCGGTGAGATGCTCTGCTTCTTACT 666
QY      221 GlyTyrGlyGluPheAspIleProLeuIleLeuThrAlaLysTyrTyrAsnAlaAspGly 240
Db      667 GGTATGCGCGATTCGATATCCCTGATCTCGATGAGCGCAAGTACTATTAACGCCATGT 726
QY      241 ThrLeuArgSerThrGluGlyGluAspGlnAspLeuTyrPyrGlyAspValIleHisValAsn 260
Db      727 ACCCTGCGCTGACCGAGGAGGTAGAGACCAAGCACTGTGGGAGATGCTATCATGTCAAC 786
QY      261 GlyGlnProTyrProPheLeuAsnValGlnProArgLysTyrArgPheArgPheLeuAsn 280
Db      787 GGACAGCAGCATGGCTTCTTCAACCTCAAGCCGCCCAAGTACCGTTCGATCTCTCAAC 846
QY      281 AlaAlaValSerArgAlaTyrPheLeuTyrLeuValArgThrSerSerProAsnValArg 300
Db      847 GCTGCGGTGTCTGCGTGTGCTCTTACCTCGTCAAGCAGCAGCTTCCCAAGCTCAGA 906
QY      301 IleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaProValGlnThrSer 320
Db      907 ATTCCTTTCCAAGTCATGCTGCTGATGCTGCTGCTTCAAGCCGCCGTCAGACCTCT 966
QY      321 AsnLeuTyrLeuAlaValAlaGluArgTyrGluIleIleIleAspPheThrAsnPheAla 340
Db      967 AACCTTACCTTGGCTGTGGCGAGCGGTACAGAGATCATTAATGACTTACCACTTTGCT 1026
QY      341 GlyGlnThrLeuAspLeuArgAsnValAlaGluThrAsnAspValGlyAspGluAspGlu 360
Db      1027 GGCCAGACTCTTGAACCTCGCAACGTTGCTGAGCAACAGATGTCGGGAGAGAGATGAG 1086
QY      361 TyrAlaArgThrLeuGluValMetArgPheValValSerSerGlyThrValGluAspAsn 380

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Db      1087 TACGCTCGCACTTCTCGAGGTGATGCCCTTCTGTCGTCAGCTGTGCACTGTGAGACAAC 1146
QY      381 SerGluValProSerThrLeuArgAspValProPheProProHisLysGluProAla 400
Db      1147 ACCGAGTCCCTTCACACTCTCGTACGTTCTTCTTCTCTTCCCTTCCACAAAGAGAGCCGCC 1206
QY      401 AspLysHisPheLysPheGluArgSerAsnGlnLysTyrLeuIleAsnAspValGlyPhe 420
Db      1207 GACAGCACTTCAATTGAAACGACGAGACGACACTACGTGATCAACGATGTTGGCTTT 1266
QY      421 AlaAspValAsnGluArgValLeuAlaLysProGluLeuGlyThrValGluValTyrPhe 440
Db      1267 GCCGATGTCAATGACCGTGTCTCGCAAGCCCGAGCTCGGACCGTTGAGTCTGGAG 1326
QY      441 LeuGluAsnSerSerGlyTyrSerHisProValHisIleHisLeuValAspPheLys 460
Db      1327 CTCGAAACTCTCTCGAGGCTGGAGCCACCCCGTCCCATTTACCTTGTGACTTCAAG 1386
QY      461 IleLeuLysArgThrGlyLysArgGlyGluIleValMetProTyrGluSerAlaGlyLeuLys 480
Db      1387 ATCTCAAGCGAACTGGTGTGTCGTCGCCAGGTGATGCTTACGATGCTGTGCTTAAG 1446
QY      481 AspValValTyrPheGlyArgGlyGluThrLeuThrIleGluAlaHisTyrGlnProTyr 500
Db      1447 GATGTCGTGTGTGGGAGGGGTGAGACCTTGACCATTCGAGGCCCTACCAACCTGG 1506
QY      501 ThrGlyAlaTyrMetTyrPheHisCysHisAsnLeuIleHisGluAspAsnAspMetAla 520
Db      1507 ACTGAGCTTACATGTGGCAGCTGTACAACTTCATTCAGAGATTAACGATGATGGCT 1566
QY      521 ValPheAsnValThrAlaMetGluGluLysGlyTyrLeuGlnLysAspPheGluAspPro 540
Db      1567 GATTCACAGTCACCGCCATGGAGGAGAAAGGATATCTTCAGAGACTTGGAGAGACCC 1626
QY      541 MetAsnProLysTyrArgAlaValProTyrAsnArgAsnAspPheHisAlaArgAlaGly 560
Db      1627 ATGAACCCCAAGTGGCGCGCTTCTTCAACACCGCAACGACTTCATGCTGCGCTGGA 1686
QY      561 AsnPheSerAlaGluSerIleThrAlaArgValGlnGluLeuAlaGluGlnLysProTyr 580
Db      1687 AACTTCTCGCGGAGATTCATCATCTGCCGAGTGCAGAGTGGCGGACAGAGAGCCGTAC 1746
QY      581 AsnArgLeuAspGluIleLeuGlnLysPheGluGlyIleGluGlu 594
Db      1747 AACCGCTCGATGAGATCTGAGGATCTTGGAAATCGAGAG 1788

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RESULT 2
 US-09-218-702-1
 ; Sequence 1, Application US/09218702
 ; Patent No. 6426410
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Huaming
 ; TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes
 ; FILE REFERENCE: GC567
 ; CURRENT APPLICATION NUMBER: US/09/218,702
 ; CURRENT FILING DATE: 1998-12-22
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1791
 ; TYPE: DNA
 ; ORGANISM: Stachybotrys sp.
 US-09-218-702-1

Alignment Scores:
 Pred. No.: 0 Length: 1791
 Score: 3189.00 Matches: 594
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatch: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-080-233-2 (1-594) x US-09-218-702-1 (1-1791)

QY 1 MetIeuPheLysSerTrpGlnIleuAlaAlaSerGlyLeuSerGlyValIleuGly 20
 DB 7 ATGCTTCAAGTCATGCGCACTGCGCAGACGCTCCGGGCTCTGCTGAGCTCCGCG 66
 QY 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40
 DB 67 ATCCCGATGAGACCGCGCAGCCACCCCATTTGAGGCTGTGATCCGAGAGGAGACTGAG 126
 QY 41 ValPheAlaAspSerIleuLeuAlaAlaGlyAspAspAspTrpGluSerProProTrp 60
 DB 127 GCTTCGTGACACCTCCCTGCTGCGAGAGCGGATGAGACGAGTGGAGTCACTCCATAC 186
 QY 61 AsnIleuLeuTrpArgAsnAlaLeuProIleProValLysGlnProLysMetIleIle 80
 DB 187 AACTTCCTTACAGGAATGCCCTGCCAATTCACCTGTACAGAGCCCAAGATGATCAT 246
 QY 81 ThrAsnProValThrGlyLysAspIleTrpTrpTrpGluIleGluIleLysProPheGln 100
 DB 247 ACCAACCCCTGTCACCGCGCAAGCATTGTGATGATGATGATGATGATGATGATGATGAT 306
 QY 101 GlnArgIleLeuTrpThrLeuArgProAlaThrLeuValGlyTrpAspGlyMetSerPro 120
 DB 307 CAAGGATTATACCCCACTGCGCCCTGCGCCTGCTGCGCTACGATGCGCATGACCCCT 366
 QY 121 GlyProThrPheAsnValProArgGlyThrGluThrValValArgPheIleAsnAla 140
 DB 367 GGTTCCTACTTCATATTTCCAGAGAGACAGAGACTGTAGTTAGTTTCATCAACAATGCC 426
 QY 141 ThrValGluAsnSerValHisIleuHisGlySerProSerArgAlaProPheAspGlyTrp 160
 DB 427 ACCGTTGAGAACCTCGGTCATCTGACGGCTCCCATCGGCTGCCCTTTCGATGGTGG 486
 QY 161 AlaGluAspValThrPheProGlyGlyTrpLysAspTrpTrpPheProAsnTrpGlnSer 180
 DB 487 GCTGAAGATGATACCTTCCCTGCGAGTACAAAGATTACTTCCCAACTCAACAATCC 546
 QY 181 AlaArgLeuLeuTrpTrpHisAspHisAlaPheMetLysThrAlaGluAsnAlaTrpPhe 200
 DB 547 GCCCGGCTCTGTGGTACCATGACACCGCTTTCATCAAGACCTCTAGAAATGCCCTATT 606
 QY 201 GlyGlnAlaGlyAlaTrpIleIleAsnAspGluAlaGluAspAlaLeuGlyLeuProSer 220
 DB 607 GGTTCAGGCTGGCGCCATCAATCAACAGCAGAGGCTGAGGATCTCTCGTCTTCTAGT 666
 QY 221 GlyTrpGlyGluPheAspIleProLeuIleLeuThrAlaLysTrpTrpAsnAlaAspGly 240
 DB 667 GGTATGGCGAGTTCGATATCCCTGATCTGACGCGCAAGTACTATTAACGCCGATGGT 726
 QY 241 ThrLeuArgSerThrGluGlyGluAspGlnAspLeuTrpGlyAspValIleHisValAsn 260
 DB 727 ACCCTGCGTTGCGAGCGAGGTGAGACGACCTGTGGGAGATGATCATTCATGTCACAC 786
 QY 261 GlyGlnProTrpProPheLeuAsnValGlnProArgLysTrpArgPheArgPheLeuAsn 280
 DB 787 GGACAGCCATGGCTTCCCTTACACGTCAGCCCGCAAGTACCGTTCCGATTCCTCAAC 846
 QY 281 AlaAlaValSerArgAlaTrpLeuLeuTrpLeuValArgThrSerProAsnValArg 300
 DB 847 GCTGCCGTGTGCTGCTGGCTGCTACCTGCTGAGGACCGCTCCCAACGTCACAG 906
 QY 301 IleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaProValGlnTrpSer 320
 DB 907 ATTCCTTCCCAAGTCAATGCTGCTGATGCTGCTGCTTCAACGCCCGCTGACACTCT 966
 QY 321 AsnLeuTrpLeuAlaValAlaGluArgTrpGluIleIleLeuAspPheThrAsnPheAla 340
 DB 967 AACCTCTACCTTGTCTTCCGAGCCTTACGAGATATTGACTTCCCAACTTGTGCT 1026
 QY 341 GlyGlnThrLeuAspLeuArgAsnValAlaGluThrAspValGlyLysGluAspGlu 360
 DB 1027 GGCAGACTCTTGACCTGCGCAACGTTGCTGAGACCAACGATGTGCGCGAGGATGAG 1086

QY 361 TyrAlaArgThrLeuGluValMetArgPheValValSerSerGlyThrValGluAspAsn 380
 DB 1087 TAGCTTCGCACTCTCGAGGATGCGCTTGTGTGCTGACGCTTGACCTGTGGAGACAC 1146
 QY 381 SerGlnValProSerThrLeuArgAspValProPheProProHisLysGluProAla 400
 DB 1147 AGCCAGTCCCTCCCACTCTCCGTGACGTTCTTTCCTCTCTCAAGAAGAGCCCGCCG 1206
 QY 401 AspLysHisPheLysPheGluArgSerAsnGlyHisTrpIleuIleAsnAspValGlyPhe 420
 DB 1207 GACAAACCTTCAAGTTTGAAACGACCAACGAGACTACCTGATCAACGATGTGGCTTT 1266
 QY 421 AlaAspValAsnGluTrpValIleuAlaLysProGluLeuGlyThrValGluValTrpGlu 440
 DB 1267 GCCGATGTCAATAGCGGTGCTTGGCCCAAGCCCGAGCTGCGCACCTGTAGGTCTGGAG 1326
 QY 441 LeuGluAsnSerSerGlyLysTrpSerHisProValHisIleHisLeuValAspPheLys 460
 DB 1327 CTCGAGAACCTCTGAGAGCTGAGCCACCCGCTCCACATTCACCTTGTGACTTCAAG 1386
 QY 461 IleLeuLysArgThrGlyArgGlyGlnValMetProTrpGluSerAlaGlyLeuLys 480
 DB 1387 ATCCTCAAGCAACTGTGGTGTGCTGGCCAGGTATGCTTACGAGTCTGTGGTCTTAAG 1446
 QY 481 AspValValTrpLeuGlyArgGlyGluThrLeuThrIleGluAlaHisTrpGlnProTrp 500
 DB 1447 GATGTGCTGTGTGGGAGAGGCTGAGACCTCTACCATGAGGCCCACTACCAACCTGG 1506
 QY 501 ThrGlyAlaTrpMetTrpHisCysHisAsnLeuIleHisGluAspAsnAspMetAla 520
 DB 1507 ACTGAGCTTACATGTGGGCTGCTGACCACTCATTCACAGAGATTAACGATGATGGCT 1566
 QY 521 ValPheAsnValThrAlaMetGluGluLysGlyTrpLeuGlnLysAspPheGluAspPro 540
 DB 1567 GTATTCAGCTCACCGCCATGAGAGAGAGGATATCTTACGAGAGACTTGCAGAGACCC 1626
 QY 541 MetAsnProLysTrpArgAlaValProTrpAsnArgAsnAspPheHisAlaArgAlaGly 560
 DB 1627 ATCAACCCCAAGTGGCGCGCTTCTTCAACCGCAGACACTTCCATGCTGCGCGTGA 1686
 QY 561 AsnPheSerAlaGluSerIleThrAlaArgValGlnGluLeuAlaGluGlnLysProTrp 580
 DB 1687 AACTTCTCGCCGAGTCCATCACTGCGCGAGTGCAGAGGTGCGCCAGAGGAGCGGTAC 1746
 QY 581 AsnArgLeuAspGluIleLeuGluAspLeuGlyIleGluGlu 594
 DB 1747 AACCGCTCGATGATCCCTGAGAGATCTTGGATGAGAG 1788

RESULT 3
 US-09-218-702-5
 ; Sequence 5, Application us/09218702
 ; Patent No. 6,426,410
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Huming
 ; TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes
 ; FILE REFERENCE: GCS67
 ; CURRENT APPLICATION NUMBER: US/09/218,702
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 2067
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: plasmid
 US-09-218-702-5

Alignment Scores:
 Pred. No.: 0
 Score: 3056.00
 Percent Similarity: 86.70%
 Best Local Similarity: 86.70%

Length: 2067
 Matches: 593
 Conservative: 0
 Mismatches: 1

Query Match: 95.83% Indels: 91
DB: 4 Gaps: 5
US-10-080-233-2 (1-594) x US-09-218-702-5 (1-2067)

QY 1 MetLeuPheLysSerTrpGluLeuAlaAlaSerGlyLeuLeuSerGlyValLeuGly 20
DB 10 ATGCTTCAAGTCAATGCAACTGGCAGACGCTCGGGCTCTCTGAGAGTCTCGGC 69
QY 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40
DB 70 ATCCGATGGACACCGGACGCCCATTTGAGGCTGTGATCCCGAAGTGAAGACTGAG 129
QY 41 ValPheAlaAspSerLeuLeuAlaAlaIaIaGlyAspAspTrpGluSerProTrp 60
DB 130 GTCCTTCGCTGACTCCCTCTCTGCTGCACAGCGCATGACACTGGAGACTCACCTCATAC 189
QY 61 AsnLeuLeu-----Tyr 64
DB 190 AACTTGCTTTACAGGTGAGACACCTGCCACCTGTTTCCCTCGATTAACCTTAAT 249
QY 65 ArgAsnAlaLeuProIleProProValLysGlnProLysMet----- 78
DB 250 AGGATGCCCTGCGCAATTCACCTGTCAAGCAGCCCAAGATGTATGCTTGATTTCTGA 309
QY 79 -----IleIleThrAsnProValThrGly 87
DB 310 CGAAGCACTCGGCCCGCACTAATGTATTTCTAGATCATTTACCAACCTGTCCAGCGCAA 369
QY 87 SASPILeTrpTyrrTyrrGluIleGluIleLysProPheGlnIaArg----- 102
DB 370 GGACATTTGGTACATAGATCGAGATCAAGCATTTACGAAAGGTGAGTTGCTCAG 429
QY 103 -----IleTyrrProThrLeuAspPr 109
DB 430 AAACCTTGCGTAATTAATCATGTTACTGACCCCTTGAGATTTACCCACCTTGCGCC 489
QY 109 oAlaThrLeuValGlyTyrrAspGlyMetSerProGlyProThrPheAsnValProArg 129
DB 490 TGCACCTCGCGCGCTACGATGGATGAGCCCTGCTCACTTCAATGTTCCAGAGG 549
QY 129 TyrrGluThrValValaArgPheIleAsnAsnAlaThrValGluAsnSerValHisLeu 149
DB 550 AACGAGACCTAGTATGATTCATCAACAAATGCCCTGGGAGAACTGGTCCATCTCA 609
QY 149 SGIserProSerArgAlaProPheAspGlyTrpAlaGluAspValThrPheProGly 169
DB 610 CGGCTCCCATCGCGCTGCTTTCGATGTTGGCTGAGATGTGACCTTCCGCGCA 669
QY 169 uTyrrLysAspTyrrTyrrPheProAsnTyrrGlnSerAlaArgLeuLeuTrpTyrrHisAsp 189
DB 670 GTACAGAGATTAACCTTCCCACTACCAATCGCCGCTTGTGTGATCCATGACACA 729
QY 189 sAlaPheMetLys----- 193
DB 730 CGCTTTCAATGAA-GGTATGCTACGAGCCCTTATCTTCTGCTGCTTGTGCTTAACCA 788
QY 194 -----ThrAlaGluAsnAlaTyrrPheGlyGlnAlaGlyAlaTyrrIleLeu 209
DB 789 CTTCCTTTGTAAGACTGTGAAATGCTTACTTTGCTAGGCTGCGCTGCTCATTTATCA 848
QY 209 nAspGluAlaGluAspAlaLeuGlyLeuProSerGlyTyrrGlyLysPheAspIlePro 229
DB 849 CGACGAGGCTGAGATGCTCGGCTTCTAGTGGCTATGCGAGTTCGATATCCCTCT 908
QY 229 uIleLeuThrAlaLysTyrrTyrrAsnAlaAspGlyThrLeuArgSerThrGlyGluAs 249
DB 909 GATCCTGAGCGCAAGTACTATAACCGCATGATACCTCGCTTGCAGACCGAGGATGAAGA 968
QY 249 pGluAspLeuTrpGlyAspValIleHisValAsnGlyLysProTrpProPheLeuAsnVal 269
DB 969 CCAGGACCTGTGGGAGATGATCATCATGTCATCAAGCAGACCATGGCTTTCCTTAACGT 1028

QY 269 IGlnProArgLysTyrrArgPheArgPheLeuAsnAlaAlaValSerArgAlaTrpLeuLe 289
DB 1029 CCAGCGCGGCAAGTACGCTTTCCGATTTCTCAAGCTCGCGTCTGCTGGCTCTCT 1088
QY 289 uTyrrLeuValArgThrSerSerProAsnValArgIleProPheGlnValIleAlaSerAs 309
DB 1089 CTACCTCGTCAGGACACACTCTCCCAAGATTCCTTCCCAAGTCAATGCTCTGCA 1148
QY 309 pAlaGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyrrLeuAlaValAlaGluAr 329
DB 1149 TGTGTGTCTCTCAAGCCCGGTTCAGACCTTAACCTTAACCTTGTGTGTGCGAGCG 1208
QY 329 TyrrGluIleIleIle----- 334
DB 1209 TTACAGATTCATTTATGTTATGCCCTCCCTCCCTCAAGATGATGATCAAGACTTAAGACT 1268
QY 335 -----AspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaG 351
DB 1269 AACACTGTACACTTCACCAACTTTCGCGCAGACTTGTACCTGCGCAACGTTGCTGA 1328
QY 351 uThrAsnAspValGlyAspGluAspGluTyrrAlaArgThrLeuGluValMetArgPheVal 371
DB 1329 GACCAAGATGTGCGCGAGAGATGATGACTGCTGCACTCTCGAGGTGATGCGCTTCT 1388
QY 371 IValSerSerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspValPr 391
DB 1389 GGTGAGTCTGGCACTGTGTGAGACACAGCAGGTCCCTCCACTCTCCGTGAGCTTCC 1448
QY 391 OPheProTrpHisLysGluGlyProAlaAspLysHisPheLysPheGluArgSerArg 411
DB 1449 TTTCCCTCTCAAGAGAGGCCCGCGAGAACACTTCAAGTTGAACACAGACAGCAGG 1508
QY 411 yHisTyrrLeuIleAsnAspValGlyPheAlaAspValAsnGluArgValIleAlaLysPr 431
DB 1509 ACACACTGTATCAACGATGTGCTTGGCTTGGCGATGTCAATAGCGTGTCTGCGCAAGC 1568
QY 431 oGluLeuGlyThrValGluValTrpGluLeuGluAsnSerSerGlyLysTrpSerHisPr 451
DB 1569 CGAGCTCGGACCGCTTGAGTCTGGAGCTCGAGAACTCTCTGGAGCTGAGCACACC 1628
QY 451 oValHisIleHisLeuValAspPheLysIleLeuLysArgThrGlyArgGlyGlnVal 471
DB 1629 GGTCCACATTCACCTTGTGACTTCAAGATCTTCAAGGAACTGCTGCTGCGCAGGT 1688
QY 471 IMeProTyrrGluSerAlaGlyLeuLysAspValValTrpLeuGlyArgGlyLysThrLe 491
DB 1689 CATGCCCTACAGATCTGCTGTGTTAAGATGTGCTGTGTTGGCAGGGGTGAGACCT 1748
QY 491 uThrIleGluAlaHisTyrrGlnProTrpThrGlyAlaTyrrMetTrpHisCysHisAsnLe 511
DB 1749 GACCATCGAGGCCCTACCAACCTGAGACTGAGACTTAACATGTGGACCTGCACAACT 1808
QY 511 uIleHisGluAspAsnAspMetMetAlaValPheAsnValThrAlaMetGluGluVal 531
DB 1809 CATTCACAGAGATTAACGATGATGCTGTTCATCAACCTCACCGCATGGAGGAGAAAGG 1868
QY 531 yTyrrLeuGlnGluAspPheGluAspProMetAsnProLysTrpArgAlaValProTyrrAs 551
DB 1869 ATATCTTAGAGAGACTTCGAGACCCCATTAACCCCAAGTGGCGGCTTCTTACAA 1928
QY 551 nArgAsnAspPheHisAlaArgAlaGlyAsnPheSerAlaGluSerIleThrAlaArgVal 571
DB 1929 CCGCAACGACTTCCATGCTCGCGTGAAACTTCTCCGCCAGATCACTGCGCGAGT 1988
QY 571 IGlnGluLeuAlaGluGlnGluProTyrrAsnArgLeuAspGluIleLeuGluAspLeuG 591
DB 1989 GCAGGAGGTGCGCAGCAGGAGCGGTACAAACCGCTGATGATCTCGGAGGATCTTGG 2048
QY 591 yTleGluGlu 594
DB 2049 AATCGAGAG 2058

RESULT 4

US-09-468-578-1
; Sequence 1, Application US/09468578
; Patent No. 6399329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; PRIORITY FILING DATE: 1999-12-21
; PRIORITY FILING DATE: 1998-12-23
; PRIORITY FILING DATE: 1998-12-23
; PRIORITY FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
09-468-578-1

Alignment Scores:
Pred. No.: 0 Length: 3677
Score: 3056.00 Matches: 593
Percent Similarity: 86.708 Conservative: 0
Best Local Similarity: 86.708 Mismatches: 1
Query Match: 95.838 Indels: 91
DB: 4 Gaps: 5

US-10-080-233-2 (1-594) x US-09-468-578-1 (1-3677)

QY 1 MetLeuPheLysSerTrpGlnLeuAlaAlaSerGlyLeuSerGlyValLeuGly 20
DB 1044 ATGCTTTAAGTACGACGCACTGCGACGACGCTCCGGCTCTGCTGAGCTCGGCT 1103

QY 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValIlyThrGlu 40
DB 1104 ATCCCGATGAGACCGCGACGCCACCCATTTAGAGCTGTGATCCCGAAGTGAAGACTGAG 1163

QY 41 ValPheAlaAspSerLeuLeuAlaAlaIleGlyAspAspAspTrpGluSerProProTyr 60
DB 1164 GCTTCGCTGACCTCCCTCTGCTGACGAGGATGACGACGAGTCCATCCTCCATAC 1223

QY 61 AsnLeuLeu-----Tyr 64
DB 1224 AACTGCTTTACAGGAGGACACCTGCCACCTGTTTCCCTCGATTAACCTCTTAT 1283

QY 65 ArgAsnAlaLeuProIleProValIlyGlnProLysMet----- 78
DB 1284 AGGAATGCCCTGCCAATTCACCTGTCAGACGCCCAAGATGTATGCTTTGATTTCTA 1343

QY 79 -----IleIleThrAsnProValIlyThrGly 87
DB 1344 CGAAGCACTCGGCCCGACCTATGTATTTCTAGAGATTCATACCACTGTCACCGGCAA 1403

QY 87 SasPIleTrpTyrTrpGluIleGluIleLysProPheGlnIleArg----- 102
DB 1404 GGACATTTGTACTATGAGATGAGATCAAGCCATTTCACCAAGAGGTGAGTTGCTCAG 1463

QY 103 -----IleTyrProThrLeuArgPr 109
DB 1464 AAACTGTGTGTAATTAATCATCTTACTGACCCCTTTCAGATTTACCCACCTTGGCCCC 1523

QY 109 OAlaThrLeuValGlyTyrAspGlyMetSerProGlyProThrPheAsnValProArgI 129
DB 1524 TCCCACTCTCGCTCGCTAGATGAGATGAGCCCTGCTCTACTTCAATGTTCCAGAG 1583

QY 129 YThrGluThrValAlaArgPheIleAsnAsnAlaTrpValGluAsnSerValHisLeuH 149
DB 1584 AACAGAGACTGATGATGATGATCAACATGACACCGTGGAGAACTCGGTCATATGGA 1643

QY 149 sGlySerProSerArgAlaProPheAspGlyTrpAlaGluAspValThrPheProGly 169

DB 1644 CGGCTCCCAATCCGCTGCCCTTCGATGGTGGGCTGAAGATGTGACTTCCCTGACGA 1703

QY 169 uTyrIlyAspTyrTrpPheProAsnTyrGlnSerAlaArgLeuLeuTrpTyrHisAspH 189
DB 1704 GTACCAAGATTTACTTCTCCCAATCAATCCGCGGCTTCTGTGTGATCATGACCA 1763

QY 189 sAlaPheMetLys----- 193
DB 1764 CGCTTTCATCAAC-GGATAGCTACGAGCCTTATCTTCTTGCTACCTTGGCTAACCA 1822

QY 194 -----ThrAlaGluAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleLeas 209
DB 1823 CTTCCTTGTGATAGCTGCTGAGATGCTTCTTGTGACAGCTGGGCCCTACATTTACAA 1882

QY 209 nAspGluAlaGluAspAlaLeuGlyLeuProSerGlyTyrGlyGluPheAspIleProle 229
DB 1883 CGACGAGGCTGAGAGATGCTCTCGCTCTCTAGTGGCTATGGGAGTTCATATCCCTCT 1942

QY 229 uIleLeuThrAlaLysTyrTrpAsnAlaAspGlyThrLeuArgSerThrGluGluAs 249
DB 1943 GATCTGACGGCCCAAGTACTATTAACGCCGATGCTACCTCTGTCACCGAGGCTGAGGA 2002

QY 249 pGlnAspLeuTrpGlyAspValIleHisValAsnGlyGlnProTrpProPheLeuAsnVa 269
DB 2003 CCAGAGACCTGTGGGAGATGTATTCATTCATCAACGCGACCAATGGCTTCTTAACGT 2062

QY 269 LglnProAlaGlyTyrArgPheArgPheLeuAsnAlaAlaValSerArgAlaTrpLeuLe 289
DB 2063 CCAGCCCGCAATACCGTTCGATTCCTCAACGCGCTGCTGCTGCTGCTGCTGCTGCT 2122

QY 289 uTyrLeuValArgThrSerSerProAsnValArgIleProPheGlnValIleAlaSerAs 309
DB 2123 CTACCTCGTAGAGACCAAGCTCTCCCAACGTCAGAAATTCCTTCCAACTTTCCTCTGA 2182

QY 309 pAlaGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGluAr 329
DB 2183 TGCTGGCTCTCTCAAGCCCGCTGACAGCTCTTAACCTTCTGCTGCTGCTGCTGCTG 2242

QY 329 gTyrGluIleIleIle----- 334
DB 2243 TTACGAGATCATTAATTAATGATGCTCCCTCCCTCCAGAAATGATCAAGAACTTAAC 2302

QY 335 -----AspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaG 351
DB 2303 AACACTGTGATGATTCACCAACTTGTGCTGCGACGCTTGTGACCTGCGCAAGTGTGTA 2362

QY 351 uThrAsnAspValGlyAspGlyAspGlyAspGlyTrpAlaArgThrLeuGluValMetArgPheVa 371
DB 2363 GACCAACGATGTGCGGAGAGATGAGTACGCTCGACATCTCGAGGTGATGCGCTTCGT 2422

QY 371 ValSerSerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspValPr 391
DB 2423 CGTCACCTCTGCGCAGCTTGTGAGACCAACACCGAGTCCCTCCACTCTCTCGTACGTTCC 2482

QY 391 oPheProProHisLysGluGluProAlaAspLysHisPheLysPheGluArgSerAsnG 411
DB 2483 TTTCCCTCTCAAGAGAGAGGCGCGCGCAAGCACTTAAGTTGAAAGCGACAGCGG 2542

QY 411 yHisTyrLeuIleAsnAspValGlyPheAlaAspValAsnGluArgValLeuAlaIlyBPr 431
DB 2543 ACACATACGTGATCAACAGATGTTGCTTCCGATGTCAATGACGATGCTCTGCGCAAGCC 2602

QY 431 oGluLeuGlyThrValGluValTrpGluLeuGluAsnSerSerGlyGlyTyrSerHisPr 451
DB 2603 CGAGCTCGGACACCGTGTGAGGTGCGAGGCTCGAAGACTCTCTGAGAGGCTGAGCAACCC 2662

QY 451 oValHisIleHisLeuValAspPheLysIleLeuLysArgThrGlyArgGlyGluVal 471
DB 2663 CGTCCACATTCACCTTGTGACTTCAAGATCCCAAGCGAACTGTGTGTGCTGCGCAAGGT 2722

QY 471 lMetProTyrGluSerAlaGlyLeuLysAspValValTrpLeuGlyArgGlyGluThrLe 491

Db 2723 CATGCCCTACGAGCTGCTGCTTAAAGAGTCTGCTGGTGGCAGGGGTGAGACCT 2782
QY 491 uThrlleGlualAhlSTyrgInProTrPhrGlAAlATyrmEtTrPhlScyHlsAnle 511
Db 2783 GACCATTGAGGCCCACTTCCACACCTGGAGCTTACATGAGCTTGACACACT 2842
QY 511 uThrlleGlualAhlSTyrgInProTrPhrGlAAlATyrmEtTrPhlScyHlsAnle 531
Db 2843 CATTCACGAGTAAAGACATGATGCTGATTAACGTCACCGCATGAGAGAGAGG 2902
QY 531 YTrleuGlIngluaSppheGluaSppheMetasnProlystrPAAlaValProTyrs 551
Db 2903 ATATCTTCAGAGAGCTTCGAGAGCCCAAGTGAAGTGGCGCGCTTCCTTACAA 2962
QY 551 nArGsnAsppheHlsAlaArgAlaGlyAsnPheserAlaGluSerIleThrAlaArgVa 571
Db 2963 CCGCAACGACTTCATGCTCGGGCGGAACCTTTCGCGGATCATACGCCGAGT 3022
QY 571 lGlnGlueuAlaGlnGlnGlnProTyrsnArGleuAspGluIleleuGluaSpleuGl 591
Db 3023 GCAGAGCTGGCGAGCAGAGACCCCTACAAACCGCTCGATGAGATCTGAGAGATCTGG 3082
QY 591 yllleGlInlu 594
Db 3083 AATCGAGGAG 3092

RESULT 5
US-09-218-702-3
; Sequence 3, Application US/09218702
; Patent No. 6,626,410
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/09/218,702
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-09-218-702-3

Alignment Scores:
Pred. No.: 0 Length: 3677
Score: 3056.00 Matches: 593
Percent Similarity: 86.70% Conservative: 0
At Local Similarity: 86.70% Mismatches: 1
Any Match: 95.83% Indels: 91
Gaps: 5

US-10-080-233-2 (1-594) x US-09-218-702-3 (1-3677)

QY 1 MetleuPheLysSerTrpGlnleuAlaAlaSerGlyLeuLeuSerGlyAlaLeuGly 20
Db 1044 ATGCTGTCAAGTCATGCACTGGCAGACGCTCGGAGCTCTCTGGAATCCTCGGC 1103
QY 21 IleProMetAspThrGlySerHisProIleGlnAlaValAspProGluValIleThrGlu 40
Db 1104 ATCCGAGTGAACACCGGAGCAGCCCATTTGAGGTGTGTAATCCGAATGAGACTGAG 1163
QY 41 ValPheAlaAspSerLeuLeuAlaAlaGlyAspAspAspTrpGluSerProProTy 60
Db 1164 GTCTTCGCTGACTCCTCTGCTGACAGGAGCATGAGACTGGAGTCACTCCATAC 1223
QY 61 AsnleuLeu-----Tyr 64
Db 1224 AACTGCTTAAAGGTGAGACACTGTCCACCTGTTTCCCTCGATACTAATCTTAT 1283
QY 65 ArgAsnAlaLeuProIleProValIleGlnProIleMet----- 78
Db 1284 AGGAATGCCCTGCCAATTCACCTGTCAAGCAGCCCAAGATGATGTATTGATTCTTA 1343

QY 79 -----IleIleThrAsnProValThrGly 87
Db 1344 CGAAGCACTGGGCCCGCAATGATATCTAGATCATTACCAACCGTGCAGCGCA 1403
QY 87 SasPileTrpTyrrGluIleGluIleLysProPheGlnArg----- 102
Db 1404 GCACATTTGGTACTATGAGATGAGATCAAGCAATTCAGCAAAAGGTGAGTTCCTAG 1463
QY 103 -----IleTyrrProThrLeuArgPr 109
Db 1464 AAACCTTGTGTAATTAATCATTTGTTACTGACCTTTGATGATTTACCCACCTCGGCC 1523
QY 109 oAlaThrLeuValGlyTyrrAspGlyMetSerProGlyProThrPheAsnValProArg 129
Db 1524 TCCCACTGCTCGGCGCTACAGAGGATGAGCGCTGCTCTACTTTCATGTTCCAGAGG 1583
QY 129 YThrGluThrValValArgPheIleAsnAsnAlaThrValGluAsnSerValHisLeuH 149
Db 1584 AACAGAGACTGATGATGATGATCATCAACATGCCCGTGGAGAACTCGCTCATCTGCA 1643
QY 149 sGlySerProSerArgAlaProPheAspGlyTrpAlaGluAspValThrPheProGly 169
Db 1644 CGGCTCCCATCGCGTCCCTTTCGATGTTGGGCTGAAGATGATGATCTCCGTCGCA 1703
QY 169 uTyrrLysAspTyrrPheProAsnTyrrGlnSerAlaArgLeuLeuTrpTyrrHisAspH 189
Db 1704 GTACAGAGATTAATCTTCCCACTACCAATCCCGCTTCTGTGTACATGAGCA 1763
QY 189 sAlaPheMetLys----- 193
Db 1764 CGCTTTCATGAA-GGTATGCTACGAGCTTATCTTCTGCTGCTTGGCTTGGCTAACCA 1822
QY 194 -----ThrAlaGluAsnAlaTyrrPheGlyGlnAlaGlyAlaTyrrIleAs 209
Db 1823 CTTCCTTCGTGATGCTGAGAAATGCTTACTTGTGTGAGCTGGCGCTTACATTAACA 1882
QY 209 nAspGluAlaGluAspAlaLeuGlyLeuProSerGlyTyrrGlyGluPheAspIlePro 229
Db 1883 CGACGAGCTGAGATGCTCTGCGTCTCTGATGCTATGAGCGATGCGATATCCCTCT 1942
QY 229 uIleLeuThrAlaLysTyrrTyrrAsnAlaAspGlyThrLeuArgSerThrGluGluAs 249
Db 1943 GATCTGTAGCGCAAGTACTATTAACCGCATGTGCTCCGCTTGACCGAGCGTGAAGA 2002
QY 249 pGlnAspLeuTrpGlyAspValIleHisValAsnGlyGlnProTrpProPheLeuAsnVa 269
Db 2003 CCAGAGACTGTGGGAGATGATCATCATGTCACGAGACAGCATGCTTCTTAACGT 2062
QY 269 lGlnProArgLysTyrrArgPheArgPheLeuAsnAlaAlaValSerArgAlaTrpLeu 289
Db 2063 CCAGCCCGCAAGTACCTTTCGATTCCTCAACGCTCCGCTGCTGCTGCTGCTCT 2122
QY 289 uTyrrLeuValArgTrpSerSerProAsnValArgIleProPheGlnValIleAlaSer 309
Db 2123 CTACCTGTCAAGAGCACTCTCCCAAGTCAAGATTCCTTCAAGTCAATTCCTCGCA 2182
QY 309 pAlaGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyrrLeuAlaValAlaGluAr 329
Db 2183 TGCTGTGCTCTCAAGCGCCGCTTCAACAGCTTAACCTTAACCTTGTGTGCGGAGCG 2242
QY 329 gTyrrGluIleIleIle----- 334
Db 2243 TTACAGAGATCAATTAATGATGCTCCCTCTCAAGATGATGATCAAGATCTTAAGACT 2302
QY 335 -----AspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaG 351
Db 2303 AACACTTGAATCACTTCACTTGTGCGCAGACTTCACTTCACTGCGCAAGCTTGA 2362
QY 351 uThrAsnAspValGlyAspGluAspGluTyrrAlaArgThrLeuGluValIleMetArgPheVa 371
Db 2363 GACCAAGATGTGCGCGCAGAGATGAGTACGCTTCGCTCGAGGTGATGCGCTTGT 2422

QY 371 lvalserSerglyThrValGluaspasnsrGlnValProSerThrLeuArgAspValPr 391
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Db 2423 CGTCACTCTGGACACTGTGGAGACAACACCGGTCCTCCACTCTCCGTACGTTCC 2482
QY 391 opheProPheHisLysGluGlyProAlaAspLysHisPheLysPheGluArgSerAsnG 411
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Db 2483 TTTCCTCTCCACAAAGAAAGGCCCGCCGACAAAGCACTTCAAGTTGAAACGCAAGCAACG 2542
QY 411 yHisThrLeuLeuAsnAspValGlyPheAlaAspValAsnGluArgValLeuAlaLysPr 431
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Db 2543 ACCTACCTGATCAACGATGTTGGCTTTGGCATGTCATGACCGTCTGCGCAAGCC 2602
QY 431 ogLeuGlyThrValGluValTrpGluLeuGluAsnSerSerglyGlyTrpSerHisPr 451
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Db 2603 CGAGCTCGGCACCGCTTGAGGTCTGGAGAGCTCGAAGCTCTCTGGAGCTGGAGCCACCC 2662
QY 451 oValHisLleHisLeuValAspPheLysLleLeuLysArgThrGlyValArgGlyGlnVa 471
|||||
Db 2663 CGTCCACATTCACCTGTGTGACTTCAAGATCCCAAGCGAAGCTGTGTGTGCGCCAGGT 2722
QY 471 lMetProGlyLysSerAlaGlyLeuLysAspValValTrpLeuGlyArgGlyLysLysPhe 491
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Db 2723 CATGCCCTACGAGACTGTGGTGTGTAAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2782
QY 491 uThrIleGluAlaHisThrGlnProTrpThrGlyAlaTrpMetTrpHisCysHisAsnLe 511
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Db 2783 GACCATCGAGGCCCATACCAACCCGAGCTGAGCTACATGTGGCAGCTGTACAACT 2842
QY 511 lLleHisGluAspAsnAspMetMetAlaValPheAsnValThrAlaMetGluLysGly 531
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Db 2843 CATTCACGAGGATAAACACATGATGCTGATTCACACGTCACCGCATGAGAGAGAAAGG 2902
QY 531 yThrLeuGlnGluAspPheGluAspPheMetAsnProLysTrpArgAlaValProGlyAs 551
|||||
Db 2903 ATATCTTCAGAGAGACTTTCAGAGACCCCAAGAACCCCAAGTGGCGCTTCCTTCAACA 2962
QY 551 nArgAsnAspPheHisAlaArgAlaGlyAsnPheSerAlaGlySerIleThrAlaArgVa 571
|||||
Db 2963 CGGCAACGACTTCCATGCTCGGCTGGAACCTCTCGCGGAGTCCATCTCCGCGAGT 3022
QY 571 lGlnGluLeuAlaGlnGlnGluProTrpArgAsnArgLeuAspGluIleLeuGluAspLeuG 591
|||||
Db 3023 GCAGAGCTGGCGCGACAGAGCCGTACAAACCCGCTGATGATGATCTGTGAGATGTGG 3082
QY 591 yIleGluGlu 594
|||||
Db 3083 AATCGAGAG 3092

ULF 6
09-468-578-6
Sequence 6, Application US/09468578
Patent No. 6,300,329

GENERAL INFORMATION:
APPLICANT: Wang, Huaming
APPLICANT: Bodle, Elizabeth A.
TITLE OF INVENTION: Phenol Oxidizing Enzymes
FILE REFERENCE: GC561-3
CURRENT APPLICATION NUMBER: US/09/468, 578
CURRENT FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 09/220, 871
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 09/338, 723
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 2063
TYPE: DNA
ORGANISM: Curvularia pallescens
US-09-468-578-6

Alignment Scores: 1.05e-201 Length: 2063
Pred. No.:

Score: 1870.00 Matches: 365
Percent Similarity: 67.62% Conservative: 82
Best Local Similarity: 55.22% Mismatches: 133
Query Match: 58.64% Indels: 82
DB: 4 Gaps: 11

US-10-080-233-2 (1-594) x US-09-468-578-6 (1-2063)

QY 2 LeuPheLysSerTrpGlnLeuAlaAlaSerGlyLeuLeuSerGlyValLeuGlyIle 21
|||||
Db 16 CTCTTCGCGCACTTCAACCTCGCTTCA -----ATTCCGAAGGCAATACGGGCTT 66
QY 22 ProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGluVal 41
|||||
Db 67 GCTTTG -----AGCGAGCTCTCTGCCAAATATATTTACCAAAACCCCGACGAAGAAAG 120
QY 42 PheAlaAspSerLeuLeuAlaAlaGlyAspAsp ----- 53
Db 121 GCTGCC -----CTGGCAGCCATCGTTGAAGATGACCCCTGCCATGTTTCAGAAATCCTG 174
QY 54 ---AspTrpGlnSerProProGlyAsnLeuLeuTrpArgAsnAlaLeuProIleProPro 72
|||||
Db 175 AAGGACTGGCAAAAGCCCGAGATATCCATCTTTTTCGCGAGGCACTGCCATCCCTCA 234
QY 73 ValLysGlnProLys ----- 77
Db 235 GCCAAGGACCGAAGTACTGATCTGAATTCATGATGACAGGTTTCTTACAAATATGCTCA 294
QY 78 -----MetIleIleThrAsnProValThrGlyLysAspIleTrpTrpGlyIle 94
|||||
Db 295 CCCATCGCAGTAAATATGACGAATCTGTCAACAAGAGAGATCTGTACTAGAGATT 354
QY 95 GluIleLysProPheGlnGlnArgGlyIleTrpProThrLeuArgProAlaThrLeuValGly 114
|||||
Db 355 GTCATCAAAACCTTTTAAACCAAGGTCATCAAGTCTTACGTCCTGCTCCCTGAGAGC 414
QY 115 TyrAspGlyMetSerProGlyProThrPheAsnValProArgGlyThrGluThrValVal 134
|||||
Db 415 TATGATGGCATTTTCACAGGCTTACGATATGTCGCGAGAGAACGAAGCCGTTGTA 474
QY 135 ArgPheIleAsnAsnAlaThrValGluAsnSerValHisLeuHisGlySerProSerArg 154
|||||
Db 475 CGATTGTTAAACAGGGGTATCCGAGAGTTCATTCATTCATGATGTTCTCCCTCCGT 534
QY 155 AlaProPheAspGlyTrpAlaGluAspValThrPheProLys ----- 168
Db 535 GCCCCCTTTGACGATGGCTGAAGATTGAT -TATGAAGGCCAATTCAAGGTACAC 593
QY 169 -----GluTrpLysAspTrp 173
Db 594 AGAACAATCTTATGATCATCAGAGTGCCCTTTTATACACACGACTCTTATAGACTAC 653
QY 174 TyrPheProAsnTrpGlnSerAlaArgLeuLeuTrpTrpHisAspHisAla ----- 190
|||||
Db 654 TACTACCGAACAACAGGCTGCCAGATCTCTGTGTACACACATCATGCTATGATGATGT 713
QY 191 -----PheMetLys 193
Db 714 GTAAGTCTTGACACTAATCATGAGCGGAAGGAAAGATCGGGCTGACACTTATAGCAG 773
QY 194 ThrAlaGluAsnAlaTrpPheGlyGlnAlaGlyAlaValTrpIleLeuAsnAspGluAlaGlu 213
|||||
Db 774 ACTGCGGAATAATCCCTTATTTGGACAGGCTGGGCGCTTACCTGATCACAGCCACGCTGAG 833
QY 214 AspAlaLeuGlyLeuProSerGlyTrpGlyGluPheAspIleProLeuIleLeuThrAla 233
|||||
Db 834 GACGCCCTCGGCTTCTCTGCGGTACGAAATATAGACATCCACATGCGTCACTAGTTC 893
QY 234 LysTrpTrpAsnAlaAspGlyThrLeuArgSerThrGluGlyLysAspGlnAspLeuTrp 253
|||||
Db 894 AAGTCTTACAAACAGTATGAACTTCCACAGAGTGGAGGAAGCAACACACTCTCTGG 953
QY 254 GlyAspValIleHisValAsnGlyLysProTrpProPheLeuAsnValGlnProArgLys 273

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Db 954 GCGGACGTCATCCATGTCACGAGCGCCGCGCATCTTCACGCTGAGCGCTGGAAG 1013
Oy 274 TYRAPHETAPHELEUASNAALALVALSERARGALETPLLEUTYLEUTYVAL 293
Db 1014 TATGCCCTTCATCTTCATATGCGGCTTTCTCGAAGCTTGGCTCTATTTGCTCAG 1073
Oy 294 THRSERPROASNAVALARGLEPROBHEGLNVALLEALASERASPLAGLYNEU 313
Db 1074 CAACAAGCACTGCTACTAGACTTCTTCCAGGTCATGGCTGTGATGACGAGGCTACTC 1133
Oy 314 GLNALAPROVALGINTHRSERASNEUTYLEUALVALALAGLUARGTYGLILE 333
Db 1134 ACGCAACCGGTCACAACTCAGATATTTACGTGGCAGCAGACGCGCTAGCAGATTCTA 1193
Oy 334 ILEASPHETHPASPHALAGLYGNTHREUSPLEUARGASNAVALALAGLUTHRAS 353
Db 1194 TTGCATCTTGGCGCTTATGACGAGCGCAGACGATAGTTGGCTTAAGTTGCAAGGCCAAT 1253
Oy 354 ASPVALGLYASPLUASPLUTYRALAARGTHREUGLUVALMETARGPHEVALSER 373
Db 1254 GGGGTGCGCACCGATGATGATGCAACACTGACAGAGTCATCGCTTCATGTCAGC 1313
Oy 374 SERGLYTHRALGLUASPASNSERGLNVALPROSERTHREUARGASVALPROPHERO 393
Db 1314 AGCCAAAGCAGTCGTGATACCTGGGTACCGCAGCAGTATCTCAGATCCAGTCCCG 1373
Oy 394 PROHISLYSGUGLYPROALASPLYSHPHELYSHPHEGLUARGSERASGLYHISTYR 413
Db 1374 GCGCAACAAACCGG---ATGACACACACTTCGCGCTTCATCGACACACAGCAGAGTGG 1430
Oy 414 LEULIENSAPVALGLYPHEALASPYALASNGLUARGVALLEUALALYSPROGLU 433
Db 1431 CGCATCAACGCGATCGGTTGTCAGACCTCCAGAACCTGATCTGGCCAAAGTACCGCGC 1490
Oy 434 GLYTHRALGLUVALTPGLUENGLUASNSERSEGLYTYTPSERHISPROVALHIS 453
Db 1491 GGCCTGTCGACCTAGTGGAGATCGAGACAGCTCGCGGCTGGTCCACCCCATTCAC 1550
Oy 454 ILEHISLEUVALASPHELYSILEULIENSARGTHRGLYG-----ARGLYGLN 470
Db 1551 GTCCACCTGTCGACTTCGAGTCGAGTCGTCGACGCTACGTCAGAACAGCACTCGCGC--- 1607
Oy 471 VALMETPROTYRGLUSERALAGLYLEULIENSAPVALVALTPLEUGLYARGLYGLUTHR 490
Db 1608 GTCAATGCCCTACGAGTCCGCGGTCTCAAGGACGTGCTGCGCGCCGACGAGACG 1667
Oy 491 LEUTHRIEGLUALHISTYRGLNPROTHRGLYALTYRMETTPHISCYSHISN 510
Db 1668 GTGCTGTCGACGACACTACGCCCCCTGGAGCGAGTCTACATGTTCCACTGCGCACAC 1727
Oy 511 LEULIENHISGLUASPASNPHEMETALALVALPHEASNAVALTHRALAMEGLULIUS 530
Db 1728 CTGATCCACGAAAGCAACATGATGCGCGCTTTCAGTACGTAAGCTCCAGAACTTT 1787
Oy 531 GLYTYRLEUGLN---GLUASPHGLUASPROMETSNPROLYSTTPARGALVALPRO 549
Db 1788 GGGTACACGACGAGCAGCGAGTTCACAGCCCGGAGTTCTCGTGTGTCGACGAGCC 1847
Oy 550 TYRASNARGASNPHEHISALARGALGLYASNPHESERALAGLUSERILLETHRAL 569
Db 1848 TTCAACCGCGCTGCTGACGCGCGATCGGGTATCTTCTCAGAACATCCATCAGGCT 1907
Oy 570 ARGVALGINTLEUALAGLUGLUPROTYRASNARGLEUASPLUILEUGLUSP 589
Db 1908 AGAGTGAACAGAGTGGGCGTGGAACACCGTACAGCAACTGGACAGGTACGCGCTCG 1967
Oy 590 LEU 590
Db 1968 CTC 1970

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RESULT 7
US-09-468-578-3

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; Sequence 3, Application US/09468578
; Patent No. 6399329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaning
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2905
; TYPE: DNA
; ORGANISM: Bipolaris splicifera
; US-09-468-578-3

Alignment Scores:
Pred. No.: 3,07e-201 Length: 2905
Score: 1868.00 Matches: 368
Percent Similarity: 67.82% Conservatve: 81
Best Local Similarity: 55.59% Mismatches: 132
Query Match: 58.58% Indels: 83
DB: 4 Gaps: 10

US-10-080-233-2 (1-594) x US-09-468-578-3 (1-2905)

Oy 2 LEUPHETYSERTTPGINTLEUALALALASERGLYLEUSERGLYVALLEGLYLE 21
Db 129 CTCCTTCAGCAGACTCAACTGCTGTCA-----ATTGGAAAGGATATACGGTGC 179
Oy 22 PROMETASPHRGLYSERHISPROILEUALALVALASPPROGLUVALTYSTHGLUVAL 41
Db 180 GCTTTG-----ACGGAAGTCCCGCCAAATTTGTGCAACACCCCGCAGAGAAAG 233
Oy 42 PHEALASERILEUVALALALAGLYASPS----- 53
Db 234 GCTGCC-----TTGGCTCAATTGTTGACATGACCTCGGATGTTGTCAACATGCTG 287
Oy 54 ---ASPTPGIUSERPROPTOYRASNLEULIENUTYRARGASNALALEUPROILEPRO 72
Db 288 AAAGACTGGCAAAACCGGAGTATCTCTATTGCGCAACACAGTCCCATCCATCCA 347
Oy 73 VALIYSGINPROLYSMETILE----- 79
Db 348 GCCAAGGAACCAAGTA-GTGAAGTTCATATCGATCGACAGGTTCTTAGAATATCTC 406
Oy 80 -----ILETHASNPVALTHRGLYASPILETPTTYRGLYLE 94
Db 407 ACCATCCACAGTAACTCAGATCTCTGTCAACAAGAGATGTACTACGAGATT 466
Oy 95 GLUILEYSRPROBHEGLNARGILETYRPROTHREUARGPROALATHREUVALGLY 114
Db 467 GTCACTAAACCTTCACACAGAGTATACCAAGCCGTGCGCTCGTTAGTAGGC 526
Oy 115 TYRASPGLYMETSERPROGLYPROTHPHEASNAVALPROARGLYTHRGILUTHVAL 134
Db 527 TATACGCACTCCCAAGGCTTACGATCATCTTGGCGGAGAGAAAGAGCTGTGTA 586
Oy 135 ARPHETLEASNAALATHVALGLUASSERVALHISLEUHSGLYSERPROSERARG 154
Db 587 CGGTTTAAACCAAGGCTGATCGCAAGAGCTCATTCATCTCCAGGCTCCCTCCCGT 646
Oy 155 ALAPROPHASPLGLYTRPAGLUASPVALTHREPROGLYGLUTYLYS----- 171
Db 647 GCCCTTTTGACGAGTGGGCTGATGATATATCATGAAGGGGGAATACAA-AGGTAGCAT 705
Oy 172 -----ASP 172

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Db	706	AGCGTGGATTCTACGATCGAAGAGCGCTCATCATCTAACAGACTTCTTCTCGAC	765
OY	173	TytrTyRhpProasnTyRgInSerAlaArgLeuLeutpTyRHisAspHisAlaPhe-Me	192
Db	766	TACTACTACCGCAACAACAACAGCTGCAGATTTTGTGTACACAGATCATGCTATGCAT	825
OY	192	t-----	192
Db	826	GTGTGTAAAGTCTTACGCACTTTTCATGTAAGTGAACGGAAGATTAAAGCTAACATCTGT	885
OY	193	-LysTThIlaGluAsnAlaTyRPhelGlyGlnAlaGlyAlaTyRtIleAsnAspGluAl	212
Db	886	GCACACCGCGCAAAAATGCTATTTCGGCGCAAGCCGGCGCTTACTGTATCACAGACCCGGC	945
OY	212	agluAspAlaLeuGlyLeuProSerGlyTyRgLyGluPhAspIleProLeuIleLeuth	232
Db	946	TGAGAGATGCTCTCGGCTCTTCAAGTTACGGAATAACACATCTCCGCTGCTCAG	1005
OY	232	fAlaLySTyRTrAsnAlaAspGlyThrLeuArgSerThGluGlyGlnAspGlnAspLe	252
Db	1006	TTCCAACTACTACAAAGCCGATGGAACTTTAAACACAGTGTGGCAAGACAAAGAGTGT	1065
OY	252	uTrIGLyAspValIleHisValaIngLyGlnProTrpProPheLeuAsnValGlnProAr	272
Db	1066	TTGGGGCGGACATCATTCCTATGTCAACGGCTACCCCTGGCATTTCTAAATGTTGAGCCTCG	1125
OY	272	gLySTyRArgPheArgPheLeuAsnAlaAlaValSerArgAlaTrpLeuLeuTyRLeuVa	292
Db	1126	AAAGTATTCGTTCTGATTCCTCAACGGGGCGTTTCAGAAACTTTCCTTACTTCGT	1185
OY	292	ArgThrSerSerProAsnValArgIleProPheGlnValIleAspAspAlaGlyLe	312
Db	1186	CAACCAAGACACACTCCACTAGCGCTTCCTTCCAGTCCATTCCTGTGATGACGAGGCT	1245
OY	312	uLeuGlnAlaProValGlnThrSerAsnLeuTyRLeuAlaValAlaGlnArgTyRGuI	332
Db	1246	ACTCAACACACCCGGGTTCAACTCAGTAATGTAATGTTGACACCCGCAACAGCCTACGAGAT	1305
OY	332	eIleIleAspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaGluTh	352
Db	1306	TGTGTGATTCGTCGGCGCTATGCGGCGCAAGCTTGATCTGGCAACTTCGCAAAAGCC	1365
OY	352	fAsnAspValGlyAspGluAspGlyTyRAlaArgThrLeuGluValMetArgPheValVa	372
Db	1366	CAAGGTATGCGGTACCGACGACGACTACGCAACACTGCAACAGGTCACTGCGTTCCAGCT	1425
OY	372	lSerSerGlyThrAlaGluAspAsnSerGlnValProSerThrLeuArgAspValProPh	392
Db	1426	CAGGAGCAACACAGTCTGCTAACTCCGCTGACCCGACAGCTATCTCAGATCCAGTGT	1485
OY	392	eProProHisLySGluGlyProAlaAspLyHisPheLyAspPheGlyuArgSerAsnGlyH	412
Db	1486	CCCCGGGACAAAAC---GACATAGACATCACTTCCGTTTCATCGTACCAAGCGGGA	1542
OY	412	sTyRLeuIleAsnAspValGlyPheAlaAspValAsnGluArgValLeuAlaLyProG	432
Db	1543	GTTGCGCATCAACCGCATCGGGTTTGCAGACAGTGCAGAACCGTGTCTTCCCAAGGTACC	1602
OY	432	uLeuGlyThrValGluValTrpGlyLeuGlyuAsnSerSerGlyLyTrpSerHisProVa	452
Db	1603	GGCGGAGTCTGTCAGGCTTTGGGAACCTTGAAACAGTCCGGCGGCTGTCCACACCCCAT	1662
OY	452	lHisIleHisLeuValAspPheLyIleLeuLyArgThrGlyValArgGlyGln-----	470
Db	1663	CCAGGTCCACCTAGTACACTTCGAGACGTCGCGACGCTTACGGCGACGAAGCATCCGCG	1722
OY	471	-ValMetProTyRGlusSerAlaGlyLeuLyAspValValTrpLeuGlyArgGlyGluTh	490
Db	1723	CGTCAATCCCTATAGGCGCGCGGCTTCAGAGAGAGTGTGTGGCTCGGCGTCCAGAGAC	1782
OY	490	fLeuThrIleGluAlaHisTyRgInProTrpThrGlyAlaTyRMetTrpHisCysHisAs	510
Db	1783	GGTCTCTGCGAACACCATATACGCCCCATAGGAGCGAGTGTCTACATGTTTCCACTGCCCAA	1842

[illegible]

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RESULT 8
US-09-401-476-1
; Sequence 1, Application US/09401476
; Patent No. 6168936
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC584
; CURRENT APPLICATION NUMBER: US/09/401,476
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1958
; TYPE: DNA
; ORGANISM: Stachybotrys Chararum
US-09-401-476-1

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Alignment Scores:	
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Score:	1630.50
Percent Similarity:	65.89%
Best Local Similarity:	54.80%
Query Match:	50.82%
DB:	4
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	Indels:
	Mismatches:
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US-10-080-233-2 (1-594) x US-09-401-476-1 (1-1958)

D5
D6

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145 AGTCCTCCCTG---GCCTTGAGGAAGGCCCTGGCGATCCCTCCTGTAAAGCGCCC 201

α // Lys-----Met-Ile11 80
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xy 00 01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

[illegible]

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

[illegible]

On 140 -----Eh~V~J~C~]~:~b~c~c~c~y~h~]~h~f~c~t~o~u~h~f~c~]~:~c~o~b~r~e~c~c~h~a~]~:~E~r~e~b~h~a~c 156

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OY 178 rGlsSerAlaArgLeuLeuTyrPheHisAspHisAlaPheMetLysThrAlaGluAsnAl 198
Db 562 GCAGGCTCCCGCAGCTTTGGTGTACATCACCATCCATGTCATCACCAGCCGGAAGACGC 621
OY 198 aTyPheGlyGlnAlaGlyAlaTyrLeuLeuAsnAspGluAspAlaLeuGlyLe 218
Db 622 CTACATGGGTGAGGCTGGTGTCTACATCATCAGACCCGCTGAGATGCCCTAACCT 681
OY 218 uProSerGlyTyrGlyGluPheAspPheProLeuLeuLeuThrAlaLysTyrTyrAsnAl 238
Db 682 CCCAGCGCGTACGCGGAGTTTGATATCCCTTGGTGTCTGATCGCAAGCGATACAGCG 741
OY 238 aAspGlyThrLeuAspSerThrGluGlyGluAspGlnAspLeuTyrPglAspValIle- 257
Db 742 AGACGGCACTCTCTTCTCCACCAATGAGAGAGTTCCAGCTTGGGTTGACGTTATCA 801
OY 257 ----- 257
Db 802 AGTGGTAGTGGAGCCCATGAGATGCTTACAGATCCTAGAACTATGATGAATG 861
OY 258 -----HisValAsnGlyGlnProTyrProPheLeuAsnValAl 270
Db 862 TGCATGCTCTAACCAAGCTCTATACAG--AACGGTAGCGCTGCTATGCTCAAGTGA 920
OY 270 nProArgLysTyrArgPheArgPheLeuAsnAlaAlaValSerArgAlaTyrPheLeuTyr 290
Db 921 GCCGCGCAAGTACCGCTTCCGCTTCTCAACCGCTCCGCTTCACCTTTCGCTGTGA 980
OY 290 rLeuValArgThrSerSerProAsnValArgIleProPheGlnValIleAlaSerAspAl 310
Db 981 TCTTGCTACCTCTGAGATTCAGAGACCAAGACTTCCCTCCAGCATTCGCGTAGAGG 1040
OY 310 aGlyLeuGlnAlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGluArgTyr 330
Db 1041 TGGTCTGCTGAGGGCTCTGTGACACCTGACACTCTGTACACTCTATGCGCGAGCTG 1100
OY 330 rGluLeuLeuLeuAspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAl 350
Db 1101 GGAGGTTTATCGACTTCTCCACTTCTGCTGCGCAGTCCATCGATCCGACACTTCC 1160
OY 350 aGluThrAsnAspValGlyAspGluAspGluTyrAlaArgThrLeuGlnValMetArgPh 370
Db 1161 TGGTCTGACGCTCGGTGTTGAGCTGAGTTGATTAACCTGACAGATCATGATGCAAT 1220
OY 370 eValValSerSerGlyThrValGlu-----AspAsnSerGlnValProSerThrLeuArg 388
Db 1221 CGTGGTTGATGAA--GTCCTTGAAGTCCGCCGACACTTCTGAGGCTGCCAACCTCCG 1277
OY 388 gAspValProPheProHisLysGluGly-----ProAla----- 400
Db 1278 AGATGTTCTTCCCTCC-----GAGGGCGGCAACTGGGAGCCCGCAAAACCCACTGA 1328
OY 401 -AspLysHisPheLysPheGluArgSerAsnGlyHisTyrLeuLeuAsnAspValGlyPh 420
Db 1329 TGACGAGACTTTCACCTTCGCGCGGCTAATGAGACAGTGAACATCAACGAGGATTA 1388
OY 420 eAlaAspValAsnGluArgValLeuAlaLysProGluLeuGlyThrValGluValTyrPgl 440
Db 1389 CTCGGATTCGAGAAACGCTGCTCCGCAATGTCGCCCGCACACTGTTGGATATGTCG 1448
OY 440 uLeuGluAsnSerSerGlyTyrPheHisProValHisIleHisIleValAspPheLys 460
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OY 460 sIleLeuLysArgThrGlyGlyArgGlyGlnValMetProTyrGluSerAlaGlyLeu 480
Db 1509 AGTCTTTCGCTGCTCACTGCCGCGGA--GTCAGACCTTATGAGGCTGCTGCTCA 1565
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OY 502 yAlaTyrMetTyrHisCysHisAsnLeuLeuHisGluAspAsnAspMetMetAlaValPh 522
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OY 522 eAsnValThrAlaMetGluGluLysGlyTyrLeuGlnGluAspPheGluAspPrometAs 542
Db 1745 CAATGTCACTGTTCGCTGAGTACTATGCTAACACTACACCGAGTTCAATGACCCATGGA 1804
OY 542 nProLysTyrArgAlaValProTyrAsnArgAsnAspPheHisAlaArgAlaGlyAsnPh 562
Db 1805 GCCTCTCTGAGAGCCCGCCCTTCTCTCTGAGAGTTCAGAAATGGCTCGGGTACTT 1864
OY 562 eSerAlaGluSerIleThrAlaArgValGlnGluLeuAlaGluGlnGluProTyrAsnArg 582
Db 1865 CAGCAGCTTGCCATCACTGACCGCATTCAGAGATGGCTAGCTTCAACCCCTACGCCCA 1924
OY 582 gLeuAspGlu 585
Db 1925 GCCTGATGAT 1934

RESULT 9
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; Sequence 3, Application US/09401476
; Patent No. 6168936
; GENERAL INFORMATION:
; APPLICANT: Wang, Huang
; TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC584
; CURRENT APPLICATION NUMBER: US/09/401,476
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Stachybotrys chararum
US-09-401-476-3

Alignment Scores:
Pred. No.: 1,95e-173 Length: 2095
Score: 1620.50 Matches: 331
Percent Similarity: 65.89% Conservative: 67
Best Local Similarity: 54.80% Mismatches: 125
Query Match: 50.82% Indels: 83
DB: 4 Gaps: 11

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Db 209 AGTCCTCCCTG---GCCTGTAGCAAGTGCCTCGCGATCCCTCTCAAGGCCGCC 265
OY 77 Lys-----Met-Ile11 80
Db 266 AAGTAGTAGTACATTCTATAGCTTACGAGAGCCAAAGCTGCTAATCATTCACAGTACCT 325
OY 80 eThrAsnProValThrGlyLysAspIleTyrTyrGluLeuGluLysProPheGlu 100
Db 326 CCCCAACCCCAACACTGAGAGACATTTGTACTACAGATGAGATTAAGCCCTTTC 385
OY 100 nGlnArgIleTyrProThrLeuArgProAlaThrLeuValGlyTyrAspGlyMetSerPr 120
Db 386 CCACAGATCACTGATCTGAGAGCCGCGCAACATGCTGTGATGATGATGATGATGCC 445
OY 120 oGlyProThrPheAsnValProArgGlyThrGluThrValValArgPheIleAsnAsnAl 140

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QY 158 pGlyTPAlaGluAspValThrPheProGlyGluTyrLysAspTyrThrPheProAsnTyr 178
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Db 686 CTACATAGGTCAGGCTGCTGCTCTACATGATGATCCAGACCGCGGAGAGATCCCTGAACT 745
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QY 238 aAspGlyThrLeuArgSerThrGluGluAspGlnAspLeuTyrGlyAspValIle-- 257
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QY 270 nProArgLysTyrArgPheArgPheLeuAsnAlaAlaValSerArgAlaThrLeuLeuTyr 290
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QY 310 aGlyLeuGluGlnAlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGluArgTyr 330
Db 1105 TGGTCTGCTGAGAGGCGCTGTTGACACTGACACTGCTGATCATGCTGATGCTGCTGCTG 1164
QY 330 rGluIleIleIleAspPheThrAsnPheAlaGluGlnThrLeuAspLeuArgAsnValAl 350
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Db 1225 TGGTCTGACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1284
QY 370 eValValSerSerGlyThrValGlu-----AspAsnSerGlnValProSerThrLeuArg 388
Db 1285 CCGCTGTTGATGAA--GTCCTTGAGTGGCGCCGACACTGCTGAGAGTCCCTCCCAACTCCG 1341
QY 388 gAspValProPheProPheHisLysGluGly-----ProAla----- 400
Db 1342 AGATGTCTCTTCCCTCC-----GAGGCGCGCAACTGCGAGACCCCAACCCCACTGCA 1392
QY 401 -AspLysHisPheLysPheGluArgSerAsnGlnYHisTyrLeuIleAsnAspValGlyP 420
Db 1393 TGCAGGACTTTCACCTTCGCGCGCTGCTATATGACAGTGGACATCAACGAGTTCACCTT 1452
QY 420 eAlaAspValAsnGluArgValLeuAlaLysProGluLeuGlyThrValGluValTyrP 440
Db 1453 CTCGAGTGTGCAAGACGCTGCTGCTCCGCAATGTCGCCCGGAGACACTGTTAGATTCGCG 1512
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QY 460 sIleLeuLysArgThrGlyGlyArgGluGlnValMetProTyrGluSerAlaGlyLeu 480
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QY 480 sAspValValThrLeuGluGlyArgGluThrLeuThrIleGluAlaHisTyrGlnProT 500
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QY 500 p-----ThrGlu 502
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QY 522 eAsnValThrAlaMetGluGluGluGlyTyrLeuGlnGluAspPheGluAspProMetAs 542
Db 1809 CATGTGACCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1868
QY 542 nProLysTyrPAlaValAlaProTyrAsnArgAsnAspPheHisAlaArgAlaGlyAsn 562
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QY 562 eSerAlaGluSerIleThrAlaArgValGlnGluLeuAlaGluGlnGluProTyrAsnArg 582
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RESULT 10
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; Sequence 8, Application US/09468578
; Patent No. 6399329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Amersporium atrum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(858)
; OTHER INFORMATION: n = A,T,C or G
US-09-468-578-8

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Best Local Similarity: 54.55% Mismatches: 65
Query Match: 20.90% Indels: 18
DB: 4 Gaps: 4

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Db 2 ACCGCGAGAAACCTTACTTGTGCTCAAGCTGCTTTCATCTGTCAGACGACCCGCTGAA 61

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: July 4, 2003, 00:18:42 ; Search time 274 Seconds

(without alignments)
3384.047 Million cell updates/sec

Title: US-10-080-233-2

Perfect score: 3189

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Scoring table: BLOSUM62

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Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 2171862

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=published.Applications.NA -QFMT=fastap -SUFFIX=rmdb -MINMATCH=0.1

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-TRANS=human40.csl -LIST=45 -DOCLALIGN=200 -THR_SCORE=pcr -THR_MAX=100

-THR_MIN=0 -ALIGN=10 -MODE=LOCAL -OUTFMT=pcr -NORM=ext -HEAPSIZE=500 -MINLEN=0

-MAXLEN=2000000000 -USER=US10080233 @cgn.1.1.160 @runatc_01072003_094524_26220

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Database: Published Applications NA:

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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	3056	95.8	2067	12	US-10-080-233-5

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6	3056	95.8	3677	12	US-10-080-210-1	Sequence 1, Appl1
7	3056	95.8	3677	12	US-10-080-233-3	Sequence 3, Appl1
8	1870	58.6	2063	12	US-10-080-210-6	Sequence 6, Appl1
9	1868	58.6	2905	10	US-09-338-723A-3	Sequence 3, Appl1
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12	1620.5	50.8	2095	9	US-09-942-185-3	Sequence 3, Appl1
13	694.5	21.8	1470	10	US-09-874-200-2204	Sequence 2204, Ap
14	666.5	20.9	858	12	US-10-080-210-8	Sequence 8, Appl1
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17	480	15.1	1707	9	US-09-938-842A-186	Sequence 186, Ap
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19	329.5	10.3	1446	9	US-10-156-761-2742	Sequence 2742, Ap
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21	322.5	10.1	669	9	US-10-156-761-751	Sequence 751, Ap
22	282	8.8	1830121	9	US-10-329-960-1	Sequence 6479, Ap
23	204	6.4	510	10	US-09-974-300-6479	Sequence 1, Appl1
24	188.5	5.9	1563	9	US-10-263-819-1	Sequence 4, Appl1
25	171.5	5.4	1500	9	US-10-164-775-4	Sequence 11, Appl1
26	162	5.1	5355	9	US-09-944-160-11	Sequence 1910, Ap
27	151	4.7	1713	9	US-09-938-842A-1910	Sequence 1675, Ap
28	147	4.6	1479	9	US-09-738-626-3280	Sequence 1626, Ap
29	147	4.6	1479	9	US-09-938-842A-1626	Sequence 1, Appl1
30	132	4.1	1764	9	US-10-002-3098-1	Sequence 89, Appl1
31	121.5	3.8	2798	12	US-10-044-090-89	Sequence 1539, Ap
32	114.5	3.6	4978	10	US-09-917-800A-1539	Sequence 1539, Ap
33	112	3.5	3700	9	US-09-938-842A-1754	Sequence 3, Appl1
34	112	3.5	1626	9	US-10-016-647-3	Sequence 483, Ap
35	106	3.3	1844	9	US-10-156-761-4583	Sequence 74, Appl1
36	105.5	3.3	1956	9	US-09-808-602-77	Sequence 77, Appl1
37	105	3.3	8797	9	US-09-808-602-77	Sequence 62, Appl1
38	105	3.3	8797	9	US-09-800-198-62	Sequence 65, Appl1
39	105	3.3	8797	9	US-10-014-436-1	Sequence 50, Appl1
40	104.5	3.3	6142	9	US-10-014-436-1	Sequence 11, Appl1
41	104.5	3.3	6142	9	US-09-423-126-11	Sequence 404, Ap
42	103.5	3.2	1791	9	US-09-975-719-104	Sequence 1, Appl1
43	102.5	3.2	3279	9	US-09-975-719-104	Sequence 1, Appl1
44	102.5	3.2	3597	9	US-09-975-719-104	Sequence 1, Appl1
45	102.5	3.2	42235	9	US-09-975-719-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-338-723A-5
Sequence 5, Application US/09338723A
Patent No. US20020019038A1
GENERAL INFORMATION:
APPLICANT: Humming, Wang
TITLE OF INVENTION: Phenol Oxidizing Enzymes
FILE REFERENCE: GCS61-2
CURRENT APPLICATION NUMBER: US/09/338-723A
CURRENT FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 09/220,871
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 1791
TYPE: DNA
ORGANISM: Stachybotrys chartarum
US-09-338-723A-5

Alignment Scores:

Pred. No.: 0
Score: 3189.00
Percent Similarity: 100.008
Best Local Similarity: 100.008
Query Match: 100.008
DB: 10
Length: 1791
Matches: 594
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-080-233-2 (1-594) x US-09-338-723A-5 (1-1791)

QY 1 MetLeuPheLysSerTrpGlnLeuAlaAlaIleSerGlyLeuLeuSerGlyValLeuGly 20
DB 7 ATGCTGTTCAAGTATGCAACTGGCACTGGACCTCGGGCTCTCTGAGATCTCTCGGC 66
QY 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40
DB 67 ATCCGATGAGACACCGGACGACCCCATGAGGCTGTGATCCGAGATGAGACTGAG 126
QY 41 ValPheAlaAspSerLeuLeuAlaAlaIleGlyAspAspAspTrpGlnSerProProtyr 60
DB 127 GCTCTCGCTGACCTCTCTCTGCTGACAGCGGATGAGACTGGGAGTCACTTCATAC 186
QY 61 AsnLeuLeuTyArgAsnAlaLeuProIleProProValLysGlnProLysMetIleIle 80
DB 187 AACTGCTTTACAGGAATGGCCCTGCCATTCACCTGTCAGACGCCAAGATGATCTT 246
QY 81 ThrAsnProValIleThrGlyLysAspIleTrpTyrgluIleGluIleLysProPheGln 100
DB 247 ACCAACCCTCTCACCGGACGACATTTGTACTATGATGATGATGATGATGATGATG 306
QY 101 GlnAlaGlyLeuTyProThrLeuArgProAlaThrLeuValGlyTyArgLysMetSerPro 120
DB 307 CAAAGGATTTACCCACCTTGGCCCTGCCACTCTCGTGGCTGACGATGGCTGAGCCCT 366
QY 121 GlyProThrPheAsnValProArgGlyThrGluThrValValArgPheIleAsnAsnAla 140
DB 367 GGTCTCACTTTCATATGTTCCAGAGACAGACAGATGATGATGATGATGATGATGATG 426
QY 141 ThrValGluAsnSerValHisLeuHisGlySerProSerArgAlaProPheAspGlyTrp 160
DB 427 ACCGTGGAGAACTGGCTCATCTGACGCTGCCATGCCCTGCTGCTGCTGCTGCTG 486
QY 161 AlaGluAspValIleThrPheProGlyGlyTyrgLysAspTyrgLysPheProAsnTyrgLys 180
DB 487 GCTGAAGTGTGACCTTCCCTGGCGAGTACAAAGATTTCTACTTCCCACTACCAATCC 546
QY 181 AlaArgLeuLeuTyrgLysAspHisAlaPheMetLysTrpAlaGluAsnAlaTyrgLys 200
DB 547 GCCCGCTTCTGTGGTACATGACGACGACCTTTCATGAGATGCTGAGAAATGCCACTT 606
QY 201 GlyGlnAlaGlyAlaTyrgLysAsnAspGluAlaGlyAspAlaLeuGlyLeuProSer 220
DB 607 GGTAGGCTGGCGCTTACATTATACACGACGAGGTGAGATGCTGCTGCTGCTGCTG 666
QY 221 GlyTyrgLysGluPheAspIleProLeuIleLeuThrAlaLysTyrgLysAlaAspGly 240
DB 667 GGTATGGCGAGTTCGATATCCCTCTGATCTGACGGCCAACTATTAACGCCGATGCT 726
QY 241 ThrLeuArgSerThrGlyGlyGluAspGlnAspLeuTrpGlyAspValIleHisValAsn 260
DB 727 ACCCTGGCTTCGACCGAGGTGAGACGACGACCTGTGGGAGATGATCATCATGTCAC 786
QY 261 GlyGlnProTrpProPheLeuAsnValGlnProArgLysTyrgLysArgPheArgPheLeuAsn 280
DB 787 GGAAGACGATGCTTCTTCTTAACGTCCAGCCGCAAGTCCGCTTCCGATTCCTCAAC 846
QY 281 AlaAlaValSerArgAlaTrpLeuLeuTyrgLysValArgThrSerSerProAsnValArg 300
DB 847 GCTGCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
QY 301 IleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaProValGlnThrSer 320
DB 907 ATTCTTTCCAAGTATGCTCTGATGCTGCTGCTCTCTCAAGCCCGCTTCAGACCTCT 966
QY 321 AsnLeuTyrgLysAlaValAlaGluArgTyrgLysIleIleIleAspPheThrAsnPheAla 340
DB 967 AACCTTCACTTGTGTGCGGACGCTTACAGATCATTAATGACTTACCAACTTGTGCT 1026
QY 341 GlyGlnThrLeuAspLeuArgAsnValAlaGluThrAsnAspValGlyAspGluAspGlu 360
DB 1027 GGGCAGACTCTTGACCTGCGCAAGCTTGTCTGAGCAACGATGTGCGGACGAGATGAG 1086

QY 361 TyrAlaArgThrLeuGluValMetArgPheValIleSerSerGlyThrValGluAspAsn 380
DB 1087 TACGCTGCACCTCTGAGAGTGTATGGCTTCCGTCGTCACACTCGGCACATGTTGAGACAAAC 1146
QY 381 SerGlnValProSerThrLeuArgAspValProPheProProHisLysGlyGluProAla 400
DB 1147 AGCCAGGTCCCTCCACTCTCCGTGACCTTCTCTCTCTCAACAAGAGGCCCTCC 1206
QY 401 AspLysHisPheLysPheGluArgSerGlnGlyHisTyrgLysIleAsnAspValGlyPhe 420
DB 1207 GACCAAGCACTTCAATTGAAAGCAGACGACACTACCTGATCAACGATGTGCTT 1266
QY 421 AlaAspValAsnGluArgValLeuAlaLysProGluLeuGlyThrValGluValTrpGlu 440
DB 1267 GCCATGTCAATGAGCGTCTCTGCGCAAGCCGACGCTGGACACCTGAGTGGAG 1326
QY 441 LeuGluAsnSerSerGlyGlyTyrgLysProValHisIleHisLeuValAspPheLys 460
DB 1327 CTCGAGAACTCTCTGAGGCTGAGCCACCCCTCCACATTCACCTTGTGACTTCAAG 1386
QY 461 IleLeuLysArgThrGlyValArgGlyGlnValMetProTyrgLysSerAlaGlyLeuLys 480
DB 1387 ATCTCAAGCGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1446
QY 481 AspValValTrpLeuGlyValGlyValThrLeuThrIleGluAlaHisTyrgLysProTrp 500
DB 1447 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1506
QY 501 ThrGlyAlaTyrgLysMetTrpHisCysHisAsnLeuIleHisGluAspAsnAspMetLys 520
DB 1507 ACTGAGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1566
QY 521 ValPheAsnValIleThrAlaMetGluGlyLysGlyTyrgLysGlnGluAspPheGluAspPro 540
DB 1567 GTATTCAACGTCACCGCATGAGAGAGATATCTTCAAGAGACTTGGAGAGACCC 1626
QY 541 MetAsnProLysTrpArgAlaValProTyrgLysAsnArgAsnAspPheHisAlaArgAlaGly 560
DB 1627 ATGAACCCCAAGTGGCGGCTGCTTCTTCAACACGCAACGATTCATGCTGCGGCTGGA 1686
QY 561 AsnPheSerAlaGluSerIleThrAlaArgValGlnGluLeuAlaGlnGluProTyrg 580
DB 1687 AACTTCTCGCGGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1746
QY 581 AsnArgLeuAspGluIleLeuGluAspLeuGlyIleGluGlu 594
DB 1747 AACCGCTCGATGAGATCTGAGAGATCTTGAATCGAGAG 1788

RESULT 2

US-10-080-210-5
; Sequence 5, Application US/10080210
; Patent No. US2002014243A1
GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; PRIORITY FILING DATE: 2002-02-19
; PRIORITY APPLICATION NUMBER: US 09/220,871
; PRIORITY FILING DATE: 1998-12-23
; PRIORITY APPLICATION NUMBER: US 09/338,723
; PRIORITY FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CDNA
US-10-080-210-5

ORGANISM: Stachybotrys sp.
US-10-080-233-1

Alignment Scores:

Pred. No.:	0	Length:	1791
Score:	3189.00	Matches:	594
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-10-080-233-2 (1-594) x US-10-080-233-1 (1-1791)

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QY 1 MetLeuPheLysSerTTPGlnLeuAlaAlaAlaSerGlyLeuLeuSerGlyValLeuGly 20
DB 7 ATGCTGTTCAAGTATGCGACACTGGACAGACCTCGGGCTCTGTCGTGGAGTCTCGGC 66
QY 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40
DB 67 ATCCCGATGGACACCGGCGACCCCAATTCAGGCTGTGATCCCGAAGTGAAGACTGAG 126
QY 41 ValPheAlaAspSerLeuLeuAlaAlaGlyAspAspTPPGLuSerProProThr 60
DB 127 GTCTTCGCTGACTCCCTCTCTGCTGACAGCGATGACGACTGGAGTCACTCCATAC 186
QY 61 AsnLeuLeuYrArgAsnAlaLeuProIleProValLysGlnProLysMetIle 80
DB 187 AACTGCTTTACAGAAATGCGCTGCATTCACCTGTCAGACAGCCCAAGATGATCAT 246
QY 81 ThrAsnProValThrGlyLysAspIleThrProValLysGlnIleLysProPheGln 100
DB 247 ACCAACCCCTGTCACCGGACAGACATTTGGTACTAGATGAGATCAACCAATTCAG 306
QY 101 GlnArgIleYrProThrLeuArgProAlaThrLeuValGlyTyrAspGlyMetSerPro 120
DB 307 CAAGAGATTACCCCACTTGGCCCTGCCACTCTCGCGGCTACGATGCGATGAGCCCT 366
QY 121 GlyProThrPheAsnValProArgGlyThrGluThrValValArgPheIleAsnAsnAla 140
DB 367 GGTCTACTTTCATGTTCCCGAGAGAACAGACTGATGATTAGTTTCATCAACATGCC 426
QY 141 ThrValGlnAsnSerValHisLeuHisGlySerProSerArgAlaProPheAspGlyTrp 160
DB 427 ACCGTGGAGACTGGTCCATCTGACAGGCTCCCATCGCGCTTCCGATGATGGTGG 486
QY 161 AlaGlnAspValThrPheProGlyLysThrLysAspTyrTyrPheProAsnThrGlnSer 180
DB 487 GCTGAAGATGACCTTCCCGGGAGAGTACAAAGATTACTTCCCACTACCAATCC 546
QY 181 AlaArgLeuLeuTyrPyrHisAspHisAlaPheMetLysThrAlaGlnAsnAlaTyrPhe 200
DB 547 GCCCGCTTGTGTGATACATGACAGACCGCTTTCATGAAAGACTGTAAGAAAGCCCTACT 606
QY 201 GlyGlnAlaGlyAlaTyrIleIleAsnAspGlnAlaGlnAspAlaLeuGlyLeuProSer 220
DB 607 GGTAGAGCTGGCGCTCACTTATACAGACAGAGCTGGAGTGGCTCTCGGCTTCTTACT 666
QY 221 GlyTyrGlyLysPheAspIleProLeuIleLeuThrAlaLysTyrTyrAsnAlaAspGly 240
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QY 241 ThrLeuArgSerThrGluGlyLysAspGlnAspLeuTrpGlyAspValIleHisValAsn 260
DB 727 ACCCTGCGTTGACCGAGGAGGAGACAGACCTGTGGGAGATGTCATCATCATGTCAAC 786
QY 261 GlyIleProTrpProPheLeuAsnValGlnProArgLysTyrArgPheArgPheLeuAsn 280
DB 787 GGAAGCGCATGGCTTCTTAAAGTCCAGCCGCAAGTACCTTCCGATTCCTCAAC 846
QY 281 AlaAlaValSerArgAlaTrpLeuLeuTyrLeuValArgThrSerSerProAsnValArg 300
DB 847 GCTGCCGTCTCTGCTGCTGCTCTACTCTCTACAGACCAAGCTCTCCCAAGCTCAGA 906
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QY 301 IleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaProValGlnThrSer 320
DB 907 ATCTCTTCCAAAGCATATGCTCTGATGCTGCTGCTCTTCAAGCCCGCTTCAGACCTCT 966
QY 321 AsnLeuTyrLeuAlaValAlaGluArgTyrGluIleIleIleAspPheThrAsnPheAla 340
DB 967 AACCTTACCTTGTGCTGGCCGACGCTTACAGATCATATATGACTTCACCACTTGTCT 1026
QY 341 GlyGlnThrLeuAspLeuArgAsnValAlaGluThrAsnAspValGlyAspGlnAspGly 360
DB 1027 GGCAGACTCTTGACTGCGGACGCTTCTGACACCAAGTCCGCGGACGAGATGAG 1086
QY 361 TyrAlaArgThrLeuGluValMetArgPheValValSerSerGlyThrValGluAspAsn 380
DB 1087 TACGCTGCACCTTCGAGAGTATGAGGCTTCTGCTGACCTTGGACAGTGTGAGAGAAC 1146
QY 381 SerGlnValProSerThrLeuArgAspValProPheProPheHisGlyGlyProAla 400
DB 1147 AGCCAGTCCCTCCACTCTCCGACGCTTCTTCCCTCCACAAAGAGGCCCGCC 1206
QY 401 AspLysHisPheLysPheGluArgSerAsnGlyHisTyrLeuIleAsnAspValGlyPhe 420
DB 1207 GACAGACCTTCAAGTTTGAACGACAGACGAGACACTACCTGATCAACGATGTGGCTTT 1266
QY 421 AlaAspValAsnGluArgValLeuAlaLysProGluLeuGlyThrValGluValTrpGlu 440
DB 1267 GCCGATGCATATGAGCGCTGCTGCGCAAGCCGACGCTGCGACGCTTGAGTCTGGAG 1326
QY 441 LeuGlnSerSerGlyLysTyrSerHisProValHisIleHisLeuValAspPheLys 460
DB 1327 CTCGAGAACTCTCTGGAGGCTGAGCCACCCCGCTCAATTCACCTTGTGACTTCAAG 1386
QY 461 IleLeuLysArgThrGlyLysArgGlyGlnValMetProTyrGlnSerAlaGlyLeuLys 480
DB 1387 ATCTCAAGCAGCACTGCTGCTGCTGCGCAGGCTACTGCTTCAAGAGTCTGCGGTCTAG 1446
QY 481 AspValValTrpLeuGlyArgGlyLysThrLeuThrIleGluAlaHisTyrGlnProTrp 500
DB 1447 GATGCTGCTGTTGGGCGAGGCTGAGACCTGACCAATCGAGGCCACTTACCAACCTGG 1506
QY 501 ThrGlyAlaTyrMetTrpHisCysHisAsnLeuIleHisGlnAspAsnAspMetAla 520
DB 1507 ACTGAGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1566
QY 521 ValPheAsnValThrAlaMetGluGluLysGlyTyrLeuGlnGlnAspPheGluAspPro 540
DB 1567 GTATTCAACGTCACCGCATGAGAGAGAGATATCTTCAAGAGACTTGCAGAGACCCC 1626
QY 541 MetAsnProLysTrpAlaGlyAlaValProTyrAsnArgAsnAspPheHisAlaArgAlaGly 560
DB 1627 ATGAACCCCAAGTGGCGCGCTTCTTACAAACGCAACGACTTCCATGCTCGCGCTGA 1686
QY 561 AsnPheSerAlaGlnSerIleThrAlaArgValGlnGluLeuAlaGlnGluGlnProTyr 580
DB 1687 AACTTCTCCCGCGATCATCTACTGCGCGAGTGTGAGAGTGTGCGCGAGAGACCTTAC 1746
QY 581 AsnArgLeuAspGluIleLeuGlnAspLeuGlyIleGluGln 594
DB 1747 AACCGCTCGATGAGATCCTGAGAGATCTTGAATCGAGAG 1788
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RESULT 4
US-10-080-233-5
Sequence 5, Application US/10080233
Patent No. US20020151450A1
GENERAL INFORMATION:
APPLICANT: Wang, Huang
TITLE OF INVENTION: NO. US20020151450A1 Phenol Oxidizing Enzymes
FILE REFERENCE: GC567
CURRENT APPLICATION NUMBER: US/10/080,233
CURRENT FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5

LENGTH: 2067
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: plasmid
US-10-080-233-5

Alignment Scores:
Pred. No.: 0 Length: 2067
Score: 3056.00 Matches: 593
Percent Similarity: 86.70% Conservative: 0
Best Local Similarity: 86.70% Mismatches: 1
Query Match: 95.83% Indels: 91
DB: 12 Gaps: 5

US-10-080-233-2 (1-594) x US-10-080-233-5 (1-2067)

1 MetLeuPheLysSerTrpGlnLeuAlaAlaSerGlyLeuLeuSerGlyValLeuGly 20
10 ATGCTGTCAAGCATGGCAACTGGCAGACCTCCGGGCTCCTGCTGGAGTCTCGGC 69
21 IleProMetAspThrGlnSerHisProIleGluAlaValAspProGluValIleThrGlu 40
70 ATCCCATGGACACCGGACACCCCACTTGAAGCTGTGATCCGAAAGTGAAGACTGAG 129
41 ValPheAlaAspSerLeuAlaAlaAlaGlyAspAspAspTrpGlnSerProProTyr 60
130 GTCTTGGCTGACTCCCTCCTGCTGCAAGCGGATGACAGCTGGAGTACCTCCATAC 189
61 AsnLeuLeu-----Tyr 64
190 AACTGCTTACAGTGAAGACACCTGTCCACCTGTTTCCCTGATTAACCTATAT 249
65 ArgAsnAlaLeuProIleProProValysGlnProLysMet----- 78
250 AGGAATGCCCTGGCAATCCACTGTCAGACACCCCAAGATGATGCTTTGATTTCTA 309
79 -----IleIleThrAsnProValIleThrGly 87
310 CGAAGACACTCGGCGCCGACTATGATTTCTAGATCATTTACCAACCTGTCCACGGCA 369
87 sasPileTrpTyrTyrGluIleGluIleLysProPheGlnGlnArg----- 102
370 GGACATTTGGTACTATGAGATCGAGATCAAGCCATTTCAAGCAAGGATGATTTGCTCAG 429
103 -----IleTyrProThrLeuArgPr 109
430 AAACCTTGGTAAATTAATCATTGTTACTGACCCCTTTCAGATTTACCCCACTGGGCC 489
109 oAlaThrLeuValIleTyrAspGlyMetSerProGlyProThrPheAsnValProArg 129
490 TGCCACTCGTCGGGTAGCATGCGATGACGCCCTGTGCTCACTTCAATGTTCCAGAG 549
129 yThrGlnThrValIleArgPheIleAsnAsnAlaThrValGluAsnSerValHisLeu 149
550 AACAGAGACTGTGTAGGTTCATCAACAATGCCACCGTAGAGAACTCGGTCCATCTGCA 609
149 sGlySerProSerArgAlaProPheAspGlyTrpAlaGluAspValIlePheProGly 169
610 CGGCTCCCATCGCGGCGCCCTTTCGATGGTGGCTGAGAGATGACCTTCCCTGGCGA 669
169 uTyrIleAspTyrTyrPheProAsnTyrGlnSerAlaArgLeuLeuTrpTyrHisAsp 189
670 GTACAGAGATTAATACTTCCCAATACCAATCGCGCGCTCTGTGTGATACATGACCA 729
189 salArpMetLys----- 193
730 CGCTTTCATGAA-GGATAGCTACGACCTTTATCTTCTGCTACCTTTGGCTAAACAA 788
194 -----ThrAlaGluAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleIleAs 209
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209 nasPGLuAlaGluAspAlaLeuGlyLeuProSerGlyTyrGlyLysPheAsnIleProle 229
849 CGACGAGGCTGAGAGATGCTCTCGTCTTCCATAGGGCTATGGAGATGATATCCCTCT 908
229 uIleLeuThrAlaLysTyrTyrAsnAlaAspGlyThrLeuArgSerThrGluGluAs 249
909 GATCTGACGCGCCAGACTATTAACCGCATGTGATACCTGCTGCGACCAAGGATGAGA 968
249 pGluAspLeuTrpGlyAspValIleHisValAsnGlyGlnProTrpProPheLeuAsn 269
969 CAGAGACTGTGGGAGATGATCAATGTCAAAGGACACCAATGGCTTTCTTCAACGT 1028
269 lGlnProArgLysTyrArgPheArgPheLeuAsnAlaAlaValSerArgAlaTrpLeu 289
1029 CAGCCCCGCAATACCGTTTCGATTTCTCAACGGCTGGCTGCTGCTGCTGGCTCT 1088
289 uTyrLeuValArgThrSerSerProAsnValArgIleProPheGlnValIleAlaSer 309
1089 CTACCTGTCAGGACCAAGCTCTCCCAACGTCAAGAAATTCCTTCCAAAGTCAATGCCCTG 1148
309 pAlaGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGlu 329
1149 TGCTGTCTCTTCAAGCCCGCTGACACTCTTAACCTGCTGCTGCTGCTGCTGCA 1208
329 gTyrGluIleIleIle----- 334
1209 TTACGAGATCATATTATGTTGATGCTCCCTCCCTCCAGCAATGATGCAAGACTAGACT 1268
335 -----AspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAla 351
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351 uThrAsnAspValIleGlyAspGluAspGlyTyrAlaArgThrLeuGlnValMetArgPhe 371
1329 GACCAACGATGTGGGAGACAGATGATGATGCTGCGACTGTGAGGTGATGGCTTCGT 1388
371 ValSerSerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspVal 391
1389 CGTCAGCTGTGGACAGTGTGAGACCAACACCAAGTCCCTCCACCTGCTGAGCTGCC 1448
391 oPheProProHisLysGlyLysProAlaAspLysHisPheLysPheGluArgSerAsn 411
1449 TTTCCCTCCACAAAGAGAGCCCGCCGCAAGCACTTCAAGTTTGCAACGCAACAGG 1508
411 yHisTyrLeuIleAsnAspValIlePheAlaAspValAsnGluArgValLeuAlaLys 431
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431 oGluLeuGlyThrValGluValIlePheGluLeuGluAsnSerSerGlyTyrPheHisPr 451
1569 CGAGCTCGGACCGCTTGAGGTCTGGAGCTCGAAGACTCTCTGGAGGCTGGAGCCACC 1628
451 oValHisIleHisLeuValAspPheLysIleLeuLysArgThrGlyGlyArgGlyGln 471
1629 CGTCCACATTCACCTTGTGACTTCAAGATCTCAAGCGCAATCGGTGGTGGCCAGGT 1688
471 lMetProTyrGlnSerAlaGlyLeuLysAspValIleTrpLeuGlyArgGlyGlnThr 491
1689 CATGCCCTACGACTGCTGCTGCTTAAAGATGCTGCTGCTGCTGCTGCTGCTGCTG 1748
491 uThrIleGluAlaHisTyrGlnProTrpThrGlyAlaTyrMetTrpHisCysHisAsn 511
1749 GACCAATGAGGCGCCACTACCAACCTGAGCTGAGTATGAGTGGACATGTCACAACT 1808
511 uIleHisGluAspAsnAspMetLeuAlaValPheAsnValIleAlaMetGluLysG 531
1809 CATTCACAGAGATTAACAGATGATGCTGATTTCAACGTCAACCGCATGAGAGAGAGG 1868
531 yTyrLeuGlnGluAspPheGluAspProMetAsnProLysTrpArgAlaValProTyr 551
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551 natGAsnAspPheHisAlaArgAlaGlyAsnPheSerAlaGluSerIleThrAlaArg 571

Db 1929 CCGCAACAGCTTCCATGCTCGGCGTGAAGAACTTCCGCCGAGTCATCAGCCCGAGT 1988
QY 571 IGLGluLeuAlaGluGluGluProTyrAsnArgLeuAspGluIleLeuGluAspLeuG1 591
Db 1989 GCAGAGCTGGCCCGCAGCAGAGCCGTACACCGCTCGATGATGATCTGGAGATCTTGG 2048
QY 591 y1leGluGlu 594
Db 2049 AATCGAGCAG 2058

RESULT 5

US-09-338-723A-1
; Sequence 1, Application US/09338723A
; Patent No. US20020019038A1
; GENERAL INFORMATION:
; APPLICANT: Humming, Wang
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-2
; CURRENT APPLICATION NUMBER: US/09/338,723A
; CURRENT FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220,871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-09-338-723A-1

Alignment Scores:

Pred. No.: 0 Length: 3677
Score: 3056.00 Matches: 593
Percent Similarity: 86.70% Conservative: 0
Best Local Similarity: 86.70% Mismatches: 1
Query Match: 95.83% Indels: 91
DB: 10 Gaps: 5

US-10-080-233-2 (1-594) x US-09-338-723A-1 (1-3677)

QY 1 MetLeuPheLysSerTrpGlnLeuAlaAlaAspGlyLeuLeuSerGlyValLeuGly 20
Db 1044 ATGGCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1103
QY 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40
Db 1104 ATCCGATGGACACCGGACAGCCCATTTGAGGCTGTGATCCGAGATGAGACTGAG 1163
QY 41 ValPheAlaAspSerLeuLeuAlaAlaAlaGlyAspAspAspTrpGluSerProTyr 60
Db 1164 GTCCTTCGCTGACTCCCTCTCTGCTGACAGCGAGTGAAGTCAAGTCAAGTCAAGTCA 1223
QY 61 AsnLeuLeu-----Tyr 64
Db 1224 AACTGGCTTTACAGGTGAGACACCTGCTCCACTGTTTCCCTCGATACCTAATCTTAT 1283
QY 65 ArgAsnAlaLeuProIleProValLysGlnProLysMet----- 78
Db 1284 AGGATGCCCTGCCAATTCACCTGTCTCAAGCAGCCCAAGATGTATGTTGATTTTCTA 1343
QY 79 -----IleIleThrAsnProValThrGlyLys 87
Db 1344 CGAAGCAACTGGGCCCGACATATGTATTTAGATCATTTACCAACCTGTCACGGCAA 1403
QY 87 sAspIleTrpTyrTrpGluIleGluIleLysProPheGlnGlnArg----- 102
Db 1404 GGACATTTGGTACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1463
QY 103 -----IleTyrProThrLeuArgPr 109
Db 1464 AAACCTGTGTATTAATCATTTGTACTGACCTTTTCAGATTATACCCACCTTGGCGCC 1523

QY 109 oAlaThrLeuValGlyTyrAspGlyMetSerProGlyProThrPheAsnValProArgG1 129
Db 1524 TGGCAGCTCTCGCGGCTACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1583
QY 129 yThrGluThrValValArgPheIleAsnAsnAlaThrValGluAsnSerValHisLeuH1 149
Db 1584 AACAGAGACTGATAGTTCATCATCAACAAGCCCACTGAGAACTGCTGCATCTGCA 1643
QY 149 sGlySerProSerArgAlaProPheAspGlyTyrPheAlaGluAspValThrPheProGlyG1 169
Db 1644 CGGCTCCCATCGCGTGGCCCTTTGATGATGATGATGATGATGATGATGATGATGATGATG 1703
QY 169 uTyrLysAspTyrTyrPheProAsnTyrGlnSerAlaArgLeuLeuTrpTyrHisAspH1 189
Db 1704 GTACAGAGATTAATCACTTCCCACTACCAATCCGCCCTTGTGTGATCATGACCA 1763
QY 189 sAlaPheMetLys----- 193
Db 1764 GCGTTTCATGAA-GGTATGCTACGAGCCCTTATCTTCTGCTACCTTTGGCTAACCAG 1822
QY 194 -----ThrAlaGluAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleLeas 209
Db 1823 CTTCCTTCTGATAGACTGCTGAGATGCTTACTTGTGCTAGGCTGGCGCTCATATATCA 1882
QY 209 nAspGluAlaGluAspAlaLeuGlyLeuProSerGlyTyrGlyGluPheAspIleProLe 229
Db 1883 CGACGAGGCTGAGATGCTCTCGCTCTCTAGTGGCTATGCGAGTTCCGATATCCCTCT 1942
QY 229 uIleLeuThrAlaLysTyrTyrAsnAlaAspGlyThrLeuArgSerThrGluGluGluAs 249
Db 1943 GATCTGAGCGCCAAAGTACTATACGCGGATGATACCTGCGTTCGACCGAGGCGAGCA 2002
QY 249 pGlnAspLeuTrpGlyAspValIleHisValAsnGlyGlnProTrpProPheLeuAsnVa 269
Db 2003 CCAGAGACTGTGGGAGATGTCATCATGTCACAGGACGACCATGCTTCTTCAAGT 2062
QY 269 IGlProArgLysTyrArgPheArgPheLeuAsnAlaAlaValSerArgAlaTrpLeuLe 289
Db 2063 CCAGCCCGCAAGTACCGTTCCTGATCTCAAGCTCCGCTCTCTGCTGCTGCTGCTGCT 2122
QY 289 uTyrLeuValArgTrpSerSerProAsnValArgIleProPheGlnValIleAsnSerAs 309
Db 2123 CTACCTGCTCAGAGACAGCTCTCCACAGTCAAGATTCCTTCCAAAGTCAATGCTCTGCA 2182
QY 309 pAlaGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGluAr 329
Db 2183 TGTGCTCTCTTCAAGCCCGCTTCAACACTTCAACTCACTTCACTTGTGTGGCGACG 2242
QY 329 gTyrGluIleIleIle----- 334
Db 2243 TTACGAGATCATTTATTTGATGCTCCCTCCCTCAAGATGATGATCAAGACTTAAAGACT 2302
QY 335 -----AspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaG1 351
Db 2303 AACACTTGTAGACTTCAACAACTTGTGGCGAGACTTGTACCTGGCGCAAGTGTGCGA 2362
QY 351 uThrAsnAspValGlyAspGluAspGluTyrAlaArgThrLeuGluValMetArgPheVa 371
Db 2363 GACCAAGCATGCTCGCGAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATG 2422
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Db 2423 CGTCAGCTGTGGACTGTTGAGGACCAAGCAGGATGCTCCCTCCACTGCTGACAGTTC 2482
QY 391 oPheProProHisLysGluGlyProAlaAspLysHisPheLysPheGluArgSerAsnG1 411
Db 2483 TTTCCTCTCTCAAGAGAGGCCCGCGAGAACACTTCAAGTTTGAGACCGACACAGCG 2542
QY 411 yHisTyrLeuIleAsnAspValGlyPheAlaAspValAsnGlyValLeuAlaLysPr 431
Db 2543 ACATCTACTGATCAACATGCTTGGCTTGGCGATGTCATATAGCGTGTGCTGGCGCAACC 2602
QY 431 oGluLeuGlyThrValGluValTrpGluLeuGluAsnSerSerGlyLysTyrSerHisPr 451

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Db 2603 CGAGCTGGCACCCTGAGGTGGAGCTCGAGACATCCCTGAGGCTGGAGCCACC 2662
Qy 451 oValHisIleHisIeuValasPheIysIleIeuLysArgThrGlyArgGlyGlnVa 471
Db 2663 CGTCCACATTCACCTTGTGTACCTCAAGATCCCAACGCAACGTGTGTGTGCGCAGGT 2722
Qy 471 lMetProTyrGluSerAlaGlyLeuLysAspValValTyrLeuGlyArgGlyGlyIle 491
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Qy 491 uThrIleGluAlaHisTyrGlnProTyrThrGlyAlaTyrMetThrPheIscysHisAsn 511
Db 2783 GACCATCGAGGCCACATACCAACCTGAGCTGAGCTTACATGTGGCAGCTGCACAACT 2842
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Db 2843 CATTCACGAGGATACGACATGATGCTGATTCACAGTCACCCCATGGAGGAGAAAGG 2902
Qy 531 YTYrLeuGlnGluAspPheGluAspPheMetAsnProLysTyrPargAlaValProTyrAs 551
Db 2903 ATATCTTCAGAGGAGACTTCGAGAGACCCCATGAACCCCAAGTGGCGCCCTTCTTCA 2962
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Qy 571 lGlnGluLeuAlaGlnGlnGlnProTyrAsnArgLysAspGluIleLeuGluAspLeuG 591
Db 3023 GCAGGAGCTGGCGAGAGAGAGCCGTACAAACCGCTCGATGATGATCTGTGAGGATCTTG 3082
Qy 591 YlIleGluGlu 594
Db 3083 AATCGAGGAG 3092

RESULT 6
US-10-080-210-1
; Sequence 1, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huang
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
US-10-080-210-1

Alignment Scores:
Pred. No.: 0 Length: 3677
Score: 3056.00 Matches: 593
Percent Similarity: 86.70% Conservative: 0
Best Local Similarity: 86.70% Mismatches: 1
Query Match: 95.83% Indels: 91
DB: 12 Gaps: 5

US-10-080-233-2 (1-594) x US-10-080-210-1 (1-3677)

Qy 1 MetLeuPheLysSerTyrGlnLeuAlaAlaLaserGlyLeuLeuSerGlyValLeuGly 20
Db 1044 ATGCTGTTCAGATGATGAGCAATGCGAGCGCTCGGCTCTGTGTGAGATGCTTGGC 1103
Qy 21 lIleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40

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Db 1104 ATCCGATGAGACACGGGAGGACCCCATTTGAGGCTGTGATCCGGAAGTAAAGATGAG 1163
Qy 41 ValPheAlaAspSerLeuLeuAlaAlaGlyAspAspTyrGluSerProProTyr 60
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Qy 61 AsnLeuLeu-----Tyr 64
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Qy 65 ArgAsnAlaLeuProIleProProValLysGlnProLysMet----- 78
Db 1284 AGGAATCCCTGCAATATTCACATGTCACAGAGCCCAAGATGATGTCTTGAATTTCTA 1343
Qy 79 -----lIleThrAsnProValThrGly 87
Db 1344 CGAAGCAACTCGGCCCGCACTAATATTCATGATATTAACCAACCTGTACACCGGCA 1403
Qy 87 sAspIleTyrTyrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 102
Db 1404 GGACATTTGGTACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1463
Qy 103 -----lIeTyrProThrLeuArgPr 109
Db 1464 AAACCTTGTGTATTAATCATATGTACTGACCTTTCAGATTTACCCACCTTGGCC 1523
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Db 1644 CGGCTCCCAATCGCGTCCCTTTCATGATGATGATGATGATGATGATGATGATGATGAT 1703
Qy 169 uTyrLysAspTyrTyrPheProAsnTyrGlnSerAlaArgLeuLeuTyrPheHisAsp 189
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Db 1823 CTTCCTTTCGAGACTGCTGAGATGCTTACTTGTGAGGCTGGCCCTACATATCA 1882
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Db 1883 CGAGGAGGTGAGATCTCTCGGTCTTCTAGTGTATGCGATGCGATGATGATGATGAT 1942
Qy 229 uIleLeuThrAlaLysTyrTyrAsnAlaAspGlyThrLeuArgSerThrGluGlyGlu 249
Db 1943 GATCTACGCGCCAGATACATATAAGCGCATGATGATGATGATGATGATGATGATGAT 2002
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Db 2063 CCAAGCCCGCAAGATCGTTTCGATTCACAGCGTGCCTGTCTGTCTGTCTGTCTGTCT 2122
Qy 289 uTyrLeuValArgThrSerSerProAsnValArgIleProPheGlnValIleAlaSerAs 309
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 QY 551 nArgAsnAspPheHisAlaArgAlaGlyAsnPheSerAlaGluSerIleThrAlaArg 571

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 QY 571 lGlnGluLeuAlaGluGlnGluProTyrAsnArgLeuAspGluIleLeuGluAsp 591
 DB 3023 GCAAGAGCTGTGGCGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3082
 QY 591 yIleGluGlu 594
 DB 3083 AATCGAGGAG 3092
 RESULT 8
 US-10-080-210-6
 ; Sequence 6, Application US/10080210
 ; Patent No. US20020142423A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Huming
 ; APPLICANT: Bodle, Elizabeth A.
 ; TITLE OF INVENTION: Phenol Oxidizing Enzymes
 ; FILE REFERENCE: GC561-3
 ; CURRENT APPLICATION NUMBER: US/10/080,210
 ; PRIOR FILING DATE: 2002-02-19
 ; PRIOR APPLICATION NUMBER: US 09/220,871
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: US 09/338,723
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 2063
 ; TYPE: DNA
 ; ORGANISM: Curvularia pallescens
 US-10-080-210-6
 Alignment Scores:
 Pred. No.: 3,1e-211 Length: 2063
 Score: 1870.00 Matches: 365
 Percent Similarity: 67.62% Conservative: 82
 Best Local Similarity: 55.22% Mismatches: 133
 Query Match: 58,648 Indels: 82
 DB: 12 Gaps: 11
 US-10-080-233-2 (1-594) x US-10-080-210-6 (1-2063)
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 QY 22 PrometAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGluVal 41
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 DB 121 GCTGCC-----CTGCGACAGCCATCGTTGAAGATGACCTGCGGATGTTTCAAGATCTG 174
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 QY 73 ValLysGluProLys----- 77
 DB 235 GCCAAGGAACGAGAGTGAAGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 294
 QY 78 -----MetIleThrAsnProValThrGlyLysAspIleTyrTyrGluIle 94
 DB 295 CCATCCGAGTAATAATGAGCAATCTGTACACAAACAGAGATCTGTACTACGAGATT 354
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 DB 355 GTATCAAAACCTTTTAAACAGAGCTTATCCAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 414
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Db      475 CGATTCGTAACCAAGGCGATCGCGAGATTCGATTCATTCCTTCATGGTTCCCTCCGT 534
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Qy      169 -----GluTrrLysaspTyr 173
Db      594 AGAACAACTTATGCATCAGGCGCTCTTTTATCTAACACAGACTCGTTTACACTAC 653
Qy      174 TyrPheProaspTyrGlnserAlaArgleuLeuTrrPrrHisaspHisAla----- 190
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Qy      191 -----PheMetLys 193
Db      714 GTAAGCTTCGACATATCATGGAGGAGCAAGCAAGATCGGCGTACACTTATGCAG 773
Qy      194 ThrAlaGluasnaAlaTrrPheGlyGlnAlaGlyAlaTrrIleleasnsPgluAlaGlu 213
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Qy      214 AspAlaLeuGlyLeuProserGlyTrrGlyLupPheaspIleProleuIleLeuThrAla 233
Db      834 GACGCCCTCGGCTCTTCCTGCGGTACGAAATACAGCATCCACTGCTGCTCGATCC 893
Qy      234 LysTrrTyrAsnaAlaaspGlyThrLeuArgSerThrGluGlyLupaspGlnaspLeuTrr 253
Db      894 AAGTTCACACACTGATGAGAACTCTCCAGACCAAGTGGGAGAACACACAGCTCTGG 953
Qy      254 GlyaspValIleHisValaspGlyGlnProTrrProPheleuAsnaValGlnProArgLys 273
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Qy      274 TyrArgPheArgPheleuAsnaAlaAlaValSerArgAlaTrrPleuLeuTrrLeuValArg 293
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Qy      414 LeuIleasnsPvalGlyPheAlaaspValAsnGluArgValLeuAlaLysProGluLeu 433
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Db      1491 GGCACGTGCGACTATGGGAACCTCGAGAACAGTCCGCGGCTGCTGCACCCATCCAC 1550
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Qy      471 ValMetProTrrGlySerAlaGlyLeuLysaspValValTrrPleuGlyArgGlyLupThr 490
Db      1608 GTCAATGCCCTACAGATCGCGCGGTCTCAAGACGTCGTGTGCTGCGCGCAGAGAGC 1667
Qy      491 LeuThrIleGluAlaHisTrrGlnProTrrPheGlyAlaTrrMetTrrHisCysHisAsn 510
Db      1668 GTGCTCGTCGAAAGCACTACGCGCCCGGACGAGTCTCAAGTTCACATGTCGCACAC 1727
Qy      511 LeuIleHisGluaspAsnMetMetAlaValPheAsnValIleAlaMetGluGluLys 530
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Qy      531 GlyTrrLeuGln---GluaspPheGluaspProMetAsnProLysTrrArgAlaValPro 549
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Qy      550 TyrAsnaLysAsnaPheHisAlaArgAlaGlyAsnPheSerAlaGluSerIleThrAla 569
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RESULT 9
US-09-338-723A-3
; Sequence 3, Application US/09338723A
; Patent No. US20020019038A1
; GENERAL INFORMATION:
; APPLICANT: Humming, Wang
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GCS61-2
; CURRENT APPLICATION NUMBER: US/09/338, 723A
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220, 871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2905
; TYPE: DNA
; ORGANISM: Bipolaris spicifera
US-09-338-723A-3

Alignment Scores:
Pred. No.: 9.07e-211 Length: 2905
Percent: 1868.00 Matches: 368
Best Similarity: 67.82% Conservative: 81
Best Local Similarity: 55.59% Mismatches: 132
Query Match: 58.58% Indels: 83
DB: 10 Gaps: 10

US-10-080-233-2 (1-594) x US-09-338-723A-3 (1-2905)
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Qy      22 PrometaspThrGlySerHisProIleGluAlaValaspProGluValIleThGluVal 41
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Db      1306  TGTGTGGATTTCGGGGCCCTATGGCGGGCAAAAGCTGGATCTGGGCAAACTTCGAAAGGC 1385
Oy      352   rAnAsPvAlcIyAsPgluAsPgluTyrAlaArgThIleuGlUvAlMetArgPheVal 372
Db      1366  CAAGGTAATGTCACCGCAGCAGCACTACGCAAAACATGCACAAAGGTATGCTTCCACGT 1425
Oy      372   1serSerGIlyThrValGluaPAsnSerGlnValProSerThrIleuArgAspValProPh 392
Db      1426  CAGCAGCCAAACACTGTCGCGATTACTCCGTCGGTAACTCCGAGCAGCTATCTCAGATCCACTT 1485
Oy      392   eProProHIsIysGlUglYProAlaAspLysHIsPheLysPheGluaRgsAsnGlyH 412
Db      1486  CCCCCGGGACAAAACC--GACATAGACCAATCACTTCGTTCCATCGTACCAACGGGGA 1542
Oy      412   sTyLeuIleuAsnAspValGlyPheAlaAspValAsnGluTyrValIleuAlaLysProG 432
Db      1543  GTGGCGCATCAACGGCATCGGGTTTGCAGACGTGCAGAACCGCTGTTCTTGGCAAGGTACC 1602
Oy      432   uLeuGIlyThrValGlUvAlTPrGlUeUgluAsnSerSerGIyLtyrTserHIsProva 452
Db      1603  GCGGGGTAAGTCTGCAGCTTTGGAACTTGAGAACAGCTCCGGCGGCTGGTGCACACCCAT 1662
Oy      452   1HIsI1eHIsIeUvAlAspPheLysI1eUeUyAlArgThIcIyglArgGlyGln----- 470
Db      1663  CCAGGTCCACCTAGTACCTTCGAGTCGACGCTGCACGCTACCGGCAAGCAAGCACTCGCGG 1722
Oy      471   -ValMetProTyrGIuSerAlaGlyLeuLysAspValValTPrLeuGlyArgGlyuTh 490
Db      1723  CGTATGCCCCATAGAGCCGCCGCTCTCAAGACGTGCTGTGGCTCGGCCCTCACAGAC 1782
Oy      490   rLeuThrTlIeGlUaHIsIyTyrGlnProTPrThrGIyAlaTyrMetTrpHIsCysHIsAs 510
Db      1783  GGTCCTCGTCCAAACACATTAACGCCCCATGGGAGCGAGGTATCAATGTTCCTCCACTGCCAA 1842
Oy      510   nLeuI1eHIsIuAspAsnAspMetMetAlaValPheAsnValThrlaMetGluGly 530
Db      1843  CCTATCCACGAACACACAGACATGATGGCCGCTTGACGTGACTTAATCCGAACCTT 1902
Oy      530   sGIlyTyTLeuGln---GIuAsPheGluAsPProMetAsnProLysTrpArgAlaValPr 549
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Oy      549   oTyAsnArgAsnAspPheHIsAlaArgAlaGlyAsnPheSerAlaGluSerTlIeThAl 569
Db      1963  TTTCACCGCGGGTATCTCAACGGCGGATCGGGTATCTTTCAAGAAGATCATCAGAGGC 2022
Oy      569   aArgValGlnGluLeuAlaGlnGlnGluProTyrAsnArgLeuAspGluI1eUeGluAs 589
Db      2023  TAGAGTAATAGTGTGGCGCTCAGACAGCCTTAACAGCAACTCCACACAAGTTACAGCTC 2082
Oy      589   pIeu 590
Db      2083  GCTC 2086

RESULT 10
US-10-080-210-3
; Sequence 3, Application US/10080210
; Patent No. US200201423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2905

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TYPE: DNA
ORGANISM: Bipolaris spicifera
US-10-080-210-3

Alignment Scores:

Pred. No.:	9,07e-211	Length:	2905
Score:	1868.00	Matches:	368
Percent Similarity:	67.82%	Conservative:	81
Best Local Similarity:	55.59%	Mismatches:	132
Query Match:	58.58%	Indels:	83
DB:	12	Gaps:	10

US-10-080-233-2 (1-594) x US-10-080-210-3 (1-2905)

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DB 129 CTCTTCAGACACTTCACACTCGTTTCA-----ATTGCGAAGGCAATATACGGTGC 179
OY 22 PrometaRhphGlySerHisProIleGlyAlaValaAspProGlyValIleGlyIle 41
DB 180 GCTTTG-----AGCGAAGTCCCGCAAAATTTGCGAACAACCCCGCAGAGAAAG 233
OY 42 PheAlaSerSerleuAlaAlaIaIaGlyAspAsp----- 53
DB 234 GCTGCC-----TTGGCTCAATTTGTGAAGTACACCTCGGAGTTGTCAACATGCTG 287
OY 54 ---AspTrpGlySerProProTyraIleuLeuTyraGAsnAlaIleuProIleProPro 72
DB 288 AAGACTGGCAAGCCCGAGTATTCCTCATTTTTCGCAACACACTGCCATCCCTCCA 347
OY 73 ValIysGlnProIysMetIle----- 79
DB 348 GCCAAGGACCAAGTA-GTAGTGTCTCAATGCGATCGACAGGTTTCTTAGAATATATC 406
OY 80 -----IleThrAsnProValThrGlyAspIleTrpTyraGlyIle 94
DB 407 AACATCCACAGTAAACTACAGATCTCTCAACAAACAGAGATGTGTACTACAGATT 466
OY 95 GluIleLysProPheGlnGlnArgIleTyraProThrLeuArgProAlaThrLeuValGly 114
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OY 115 TyraSpGlyMetSerProGlyProThrPheAsnValProArgGlyThrGluThrValVal 134
DB 527 TATAGCGGATCTCCCGAGTCTCAAGTCAATAGGCGGAGAGAACAGACTGTGTA 586
OY 135 ArgPheIleAsnAsnAlaThrValGluAsnSerValHisLeuHisGlySerProSerArg 154
DB 587 CGGTTTAAACACAGGATGATCGGGAAGCTCCATCCATCTCCAGGCTCCCGCCGT 646
OY 155 AlaProPheAspGlyTrpAlaGluAspValThrPheProGlyGluTyraLys----- 171
DB 647 GCCCCTTTTGAAGGATGGGTGATGATGATCATGAAGGGGAATACAA-AGTATACAT 705
OY 172 -----Asp 172
DB 706 AGCGTGATCTTACGCATCGACAGAACCTTATCATATAACAGACTTTTCTTACAGAC 765
OY 173 TyTrpPheProAsnTyraGlnSerAlaArgLeuLeuTrpTyraHisAspHisAlaPhe-Me 192
DB 766 TACACACCGCAGAAATATGCTATTTTCGGGCAAGCCGGCCCTACCTGATCAACAGCCGCG 945
OY 192 t----- 192
DB 826 GTTGTAAAGCTTTTACCGACTTTTCATGCTAGTGAACGGAAGATTAAAGTAAATCTGT 885
OY 193 -LysThrAlaGluAsnAlaTyraPheGlyGlnAlaGlyAlaTyraIleIleAsnAspGluAl 212
DB 886 GCAACACGCAAAATATGCTATTTTCGGGCAAGCCGGCCCTACCTGATCAACAGCCGCG 945
OY 212 agIAspAlaLeuGlyLeuProSerGlyTyraGlyGluPheAspIleProLeuIleLeuTh 232
DB 946 TAGAGATGCTCTCGGCTTCTTCAAGTTACGGAAATATAGACATTCGGCTGCTCTAG 1005
```

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OY 232 fAlaLysTyTrpTyraAsnAlaAspGlyThrLeuArgSerThrGluGluAspGlnAspLe 252
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OY 252 uTrpGlyAspValIleHisValAsnGlyGlnProTrpProPheLeuAsnValGlnProAr 272
DB 1066 TTGGGGCAGCATCATCCATGTCACAGCGTCAACCCCGCCCATCTTAAATGTTGAGCCTCG 1125
OY 272 gLysTyraRhphLeuArgPheLeuAsnAlaAlaValSerArgAlaTrpLeuLeuTyraLeu 292
DB 1126 AAAGATGCTTTCATTCCTCAACGGCGGTGTTTCTAGGAACCTTGCCCTTACCTTCGT 1185
OY 292 lArgTrpSerSerProAsnValArgIleProPheGlnValIleAserAspAlaGlyIle 312
DB 1186 CAAGAACACAAACACTGCGACACTAGAGCTTCCTTCCAGGTCAATGCTGTGATGCGAGGCT 1245
OY 312 uLeuGlnAlaProValGlnThrSerAsnLeuTyraLeuAlaValaIaGluArgTyraGluI 332
DB 1246 ACTCACACACCCCGGTTCAAACTCAGATATGATGTTCCACCCCGCAGAACCTCAGAGAT 1305
OY 332 eIleIleAspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValaIaGluTh 352
DB 1306 TGTGTTCATTTTCGCGCCCTATGCGCGCAAACTGTGATGTGCGCAACTTCGCAAAAGC 1365
OY 352 fAsnAspValGlyAspGluAspGlyTyraAlaArgThrLeuGluValaIleTarGrpHeVal 372
DB 1366 CAATGTGATCGGTACCGCAGCAGACTACGCAAAACACTGACAGAGTCAATGCTTCCACAGT 1425
OY 372 lSerSerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspValProPh 392
DB 1426 CAGCAGCAAAACAGTCTGATTAACCTCGGTGATCCGACGAGCTATCTCAGATCAAGTT 1485
OY 392 eProProHisLysGluGlyProAlaAspLysHisPheLysPheGluArgSerAsnGlyI 412
DB 1486 CCCCGGCGCAAAAC--GACATAGACATCACTCTCGTTCCATGCTACCAACGGCGA 1542
OY 412 sTyraLeuIleAsnAspValGlyPheAlaAspValaIaAsnGluArgValaLeuAlaLysProG 432
DB 1543 GTGGCGCATCAACGCGATCGGGTTGCGAGAGTGCAGAACCGTGTCTTCCCAAGATACC 1602
OY 432 uLeuGlyThrValGluValTrpGluLeuGluAsnSerSerGlyTyraTrpSerHisProVa 452
DB 1603 GCGGCTACTCTGCAAGCTTTTGGAACTTGAACAGCTCCGCGGCTGTGCACCCCAT 1662
OY 452 lHisIleHisLeuValaAspPheLysIleLeuLysArgThrGlyArgGlyGln----- 470
DB 1663 CCAGCTCACCTAGTACTTCCAGATGCTGCGACCGCAGCGCAAGGCAAGGCACTCGCGG 1722
OY 471 -ValMetProTyraGluSerAlaGlyLeuLysAspValaIaTrpLeuGlyArgGlyGluTh 490
DB 1723 CGTATGCGCTTATGAGCGCGCGGCTCAGAGAGCTGCTGCGCGCTCCAGAGAC 1782
OY 490 fLeuThrIleGluIleHisTyraGlnProTrpThrGlyAlaIaTyraMetTrpHisCysHis 510
DB 1783 GGTCTCGTGCAGACATTTACGCCCAATGGAGCGAGGCTCAATGTTCACCTCCACAA 1842
OY 510 nLeuIleHisGluAspAsnAspMetMetAlaValaIaPheAsnValaIaIaMetGluGly 530
DB 1843 CCTATCCAGCAAAACACAGACATGATGGCGGCTTGACAGTAACTCAAGCACTT 1902
OY 530 sGlyTyraLeuGln---GluAspPheGluAspPrometaAsnProLysTrpArgAlaValPr 549
DB 1903 TGGGTACACAGACAGCATGATTTCCAGATCTCGAGAGATCTCGGTGTCAGACAAACC 1962
OY 549 oTyraAsnArgAsnAspPheHisAlaArgAlaGlyAsnPhSerAlaIaIaSerIleThrAl 569
DB 1963 TTTTACCGCGGGTATCTCAGCGGCGATGGGATCTTTTCAAAATCCATCAACAGGC 2022
OY 569 aArgValGlnGluLeuAlaGluGlnGluProTyraAsnArgLeuAspGluIleLeuGluAs 589
DB 2023 TAGAGTAAATGATGTGGCGCTTCAGACAGCTTACAGCAACTCCACACAGTATACAGCTC 2082
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QY	589	pleu	590
Db	2083	GCTC	2086

Search completed: July 4, 2003, 02:23:25
Job time : 349 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 3, 2003, 22:50:57 ; Search time 2297 Seconds

(without alignments)
4188.123 Million cell updates/sec

Title: US-10-080-233-2

Perfect score: 3189

Sequence: 1 MFKSMQLAASGLSCVLTG.....AEQEPYRLELDLGGEE 594

Scoring table:

BIOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n model -DEV=rlh
-Q/cgn2.1/USPTO.spool/US10080233/runat_01072003_094519_26108/app_query.fasta.1.775
-DB=EST -QMT=fastap -SUFFIX=1st -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=BIOSUM62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=10 -MOD=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USPR=US10080233 @CGN 1.1.1906 @runat_01072003_094519_26108 -NCPU=6 -ICPU=3
-NO_MMP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSRBLCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	355.5	11.1	600	10 BE188240	BE188240 M7ATIG In
2	355.5	11.1	700	10 BE187716	BE187716 B10X In
3	305.5	9.6	706	10 AW774671	AW774671 EST33822
4	296.5	9.3	848	10 BE216983	BE216983 EST0376 T
5	293.5	9.2	739	14 BO866278	BO866278 OGC7113.Y
6	290.5	9.1	592	13 BM143324	BM143324 S3J42510
7	283.5	8.9	1128	17 AF094955	AF094955 AF094955
8	277.5	8.7	563	13 BM519618	BM519618 sak81e01
9	256.5	8.0	766	12 BG526127	BG526127 56-88 Ste
10	236	7.4	465	12 BG053739	BG053739 RH12.9.B
11	229.5	7.2	599	12 BF258534	BF258534 HVMFE001
12	221	6.9	782	12 BF257494	BF257494 HY_CEA001
13	220	6.9	664	10 BE188099	BE188099 CFC377-R
14	212.5	6.7	580	13 BJ159802	BJ159802 BJ159802
15	209	6.6	714	14 BU025469	BU025469 QHF9121.Y
16	208.5	6.5	456	9 A1488265	A1488265 EST246587
17	208	6.5	713	14 BO916926	BO916926 QHB1404.Y
18	208	6.5	717	14 BO971392	BO971392 QHB6M24.Y
19	208	6.5	720	14 BU025741	BU025741 QHG11C24
20	208	6.5	750	14 BO970636	BO970636 QHB42K15
21	205	6.4	786	14 BU025791	BU025791 QHG11H04
22	204	6.4	597	14 BO849512	BO849512 QGB10B15
23	202	6.3	725	14 BO970480	BO970480 QHB42P07
24	201	6.3	725	14 BO970351	BO970351 QHB41M24
25	200.5	6.3	447	17 BH864257	BH864257 SALK_0956
26	196	6.1	693	14 BO965570	BO965570 QHB22E15
27	195	6.1	683	14 BO971750	BO971750 QHB8D22.Y
28	195	6.1	695	14 BU023825	BU023825 QHF14A05
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32	188	5.9	681	14 BO915453	BO915453 QHB14K10
33	188	5.9	690	14 BO915421	BO915421 QHB14I18
34	188	5.9	699	14 BO965695	BO965695 QHB22L02
35	187	5.9	726	14 BO971294	BO971294 QHB6H18.Y
36	186	5.8	665	14 BO971648	BO971648 QHB7M11.Y
37	184	5.8	636	14 BU024818	BU024818 QHF6D21.Y
38	184	5.8	645	14 BO965503	BO965503 QHB22B06
39	184	5.8	695	14 BO967332	BO967332 QHB29K19
40	183	5.7	574	14 BO915108	BO915108 QHB13F23
41	183	5.7	630	14 BO914488	BO914488 QHB10L17
42	181	5.7	622	14 BO967966	BO967966 QHB32P19
43	181	5.7	673	14 BO970459	BO970459 QHB42C08
44	181	5.7	681	14 BU023296	BU023296 QHF10G01
45	181	5.7	689	14 BO970978	BO970978 QHB5H07.Y

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION M7ATIG in vitro expressed cDNAs Cladosporium fulvum EST 25-SEP-2000
Bilirubin oxidase precursor, mRNA sequence.
ACCESSION BE188240
VERSION
KEYWORDS BE188240.1 GI:8667479
SOURCE
ORGANISM Cladosporium fulvum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et
Chaetothyrionomycetes incertae sedis; Mycosphaerellaceae; mitosporic
Mycosphaerellaceae; Cladosporium.
REFERENCE
1 (bases 1 to 600)
Clark,A.J., Rasmussen,S.W. and Oliver,R.P.

TITLE	In vitro expressed genes of <i>Cladosporium fulvum</i>
JOURNAL	Unpublished (2000)
COMMENT	Contact: R.P.Oliver

FEATURES	Location/Qualifiers
source	1. .600

Alignment Scores:	
Pred. No.:	1,75e-26
Score:	35.50
Percent Similarity:	58.33%
Best Local Similarity:	46.08%
Query Match:	11.15%
AB:	10
Length:	600
Matches:	94
Conservative:	25
Mismatches:	72
Indels:	15
Gaps:	4

US-10-080-233-2 (1-594) x BE188240 (1-600)

[illegible]

Db.	529	CGAAGTCACACCAATGATGGCCCCGGCTTCAACACGACACCTTGAACGGCTGAGCTACGAC	588
Qy	533	eugInglu 535	
Db	589	:::	
		TTTCAACAG 596	

RESULT 2	LOCUS	DEFINITION
BE187716	700 bp	EST 25-SEP-2000
BE187716	mRNA	linear
BI10X	in vitro expressed cDNAs	Cladosporium fulvum cDNA similar to
Bilirubin oxidase precursor, mRNA sequence.		

ACCESSION	BE187716	GI:8666955
VERSION	BE187716.1	
KEYWORDS	EST.	
SOURCE	<i>Cladosporium fulvum</i> .	
ORGANISM	<i>Cladosporium fulvum</i>	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes at Chaetothyrionomycetes incertae sedis; Mycosphaerellaceae; mitosporia
Mycosphaerellaceae; Cladosporium.
1 (bases 1 to 700)
Clark, A.J., Rasmussen, S.W. and Oliver, R.P.
In vitro expressed genes of Cladosporium fulvum
Unpublished (2000)
Contact: R.P. Oliver

FEATURES	Location/Qualifiers
source	1. .700

BASE COUNT	158 a	206 c	183 g	146 t	7 others
ORIGIN					

Alignment Scores:	
Pred. No.:	2,25e-26
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Best Local Similarity:	45.58%
Query Match:	11.15%
	Length: 700
	Matches: 98
	Conservative: 28
	Mismatches: 74
	Indels: 18

US-10-080-233-2 (1-594) X BE187716 (1-700)

[illegible]

Db : 231 GACCGTCATAGCGCGTGGATTTCAGACCGACCGACGCTGCTGCTAGCGCCACA 290
433 ugiThnValGluValTrpGluLeuGlnSerSerGlyGlyTrpSerHisProValH1 453
291 AGGCACTGTCGCGTGGCGCTGTCGACACTGGCGCTGCGCTGTCACACCGACGACA 350
Qy 453 sileHsLeuValAspPheGlyLeuLysArgThrGlyGlyArgGlyGlnValMetPr 473
351 TATCCATCTGTGTAACATGACGAGGCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTG 410
Qy 473 oYrGluSerAlaGlyLeuLysAspValValTrpLeuGlyArgGlyGlyLeuThrH1 493
411 ATACGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 470
Qy 493 egluAlaHsTyGlnProThrGlyAlaTyMetTrpHisCysHisLeuLeuH1 513
471 GCTTGGCTTTTACGGCTTGGACGCGCTTGAC-ATGCTTCATTTGACAC-CTTGTACA 528
Db 513 sgluAspAsnAspMetMetAla-ValPheAsnValThrAlaMetGluGlyGlyTyrL 533
529 CGAAGATACACCATGATGCGCGCTGTCACACGACGACGACGCTGACGCTGCTGACG 588
Qy 533 euGlnGlu-----AspPheGluAspProMetAsnProLys 544
589 TTCACAGACGACGACGCTTGGC-GAACCAATGATGATCCGACA 628

RESULT 3
AM774671 706 bp mRNA linear EST 07-SEP-2000
LOCUS
DEFINITION EST33822 RV3 Medicago truncatula cDNA clone pKV3-23H7, mRNA
SEQUENCE
AM774671
VERSION
KEYWORDS
SOURCE
ORGANISM
barrel medic.
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 706)
VandenBosch,K., Hurt,J., Moore,J., Beremand,P., Peng,H., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
ESTs from roots of Medicago truncatula after Rhizobium inoculation
unpublished (1999)
Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenb@cds.umn.edu
Texas A&M EST name: T258090e
TIGR sequence name: MTEBE40TK
More information is available at:
http://chrysis.tamu.edu/medicago
Seq primer: Skmod (CTA gaa cta gtc gat cc).
Location/Qualifiers
1..706
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/cultivar="genotype A17"
/db_xref="taxon:3880"
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/clone_1ib="KV3"
/tissue_type="Seedling roots"
/dev_stage="3 days post-inoculation with Sinorhizobium
meliloti"
/lab_host="E. coli strain XL0R"
/note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the UniZap XR vector from

FEATURES
source

Stratagene and packaged using GigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-assist
helper phage and propagated in XL0R cells.

BASE COUNT 203 a 154 c 138 g 211 t
ORIGIN
Alignment Scores:
Pred. No.: 3,51e-21 Length: 706
Score: 305.50 Matches: 83
Percent Similarity: 46.91% Conservative: 31
Best Local Similarity: 34.16% Mismatches: 84
Query Match: 9.58% Indels: 45
DB: 10 Gaps: 9
US-10-080-233-2 (1-594) x AM774671 (1-706)
Qy 146 ValHsLeuHsGlySerProSerArgAlaProPheAspGly----- 159
Db 14 GTTCATCTCCACGCGTGAATTCAGAACCGAAGCGATGTAACCCAACTCATTTTC 73
Qy 160 -----TrpAlaGluAspValThrPheProGlyGlu 169
Db 74 ACCGCTGATTCAAATCAAGGACCCACTTGGACAAA----- 112
Qy 170 TyrLysAspTyrTyrPheProAsnTyrGlnSerAlaArgLeuLeuTyrPyrHisAspHis 189
Db 113 ---AAGTCATATCTCCTTCCTCAATATCAACACCCCTGGAATTTATGTACATGACAT 169
Qy 190 AlaPheMetLysThrAlaGluAsnAlaTyrPheGlyGlnAlaGlyAlaTyrLeuLeuAsn 209
Db 170 GCTATGGCTTTCACGACGACGACGACGCTTACGCTGCTTAAATGGACCTCATCATTCGT 229
Qy 210 AspGluAla---GluAspAlaLeuGlyLeuProSerGlyTyrGlyGluPheAspPhePro 228
Db 230 GACCTTCGATTCGATCAACGCTAAATTCACACACGCT---AAGCAATTCGATTTACCG 286
Qy 229 LeuLeuLeuThrAlaLysTyrTyrAsnAlaAspGlyThr-----LeuArgSerThrGlu 246
Db 287 TTGATGTATTCATTCATCTGATGCTTTAAACGACGCTGATTCATGAACTCAACTGCT 346
Qy 247 GlyGlu-----AspGlnAspLeuTrpGlyAspValLeuHsVal 259
Db 347 AACAAACCTTCGATTCATCCACAGTGCACACCGGAATATTTGGTGCACGATCATGTGA 406
Qy 260 AsnGlyGlnProTyrProPheLeuAsnValGlnProArgLysTyrArgPheAspGlyLeu 279
Db 407 AACGTTAAAGCTTGGCCACGCTTAACTGACGAGCTGTAAGATTAATTCGATCATC 466
Qy 280 AsnAlaAlaValSerArgAlaTrpLeuLeuTyrLeuValArgThrSerProAsnVal 299
Db 467 ATTCGAAGTACGCTACATTTTTCAGGCTCTTTTC-----AGTAATGCTTTA 514
Qy 300 ArgLeuProPheGlnValLeuLeuSerAspAlaGlyLeuGlnAlaProValGlnThr 319
Db 515 AGA-----TTTGNACAGCTGGCATTCGATTCCTATATTCGGGAAGCAGGTACAGGT 568
Qy 320 SerAsnLeuTyrLeuAlaValAlaGluArgTyrGlnLeuLeuLeuAspPheThrAspPhe 339
Db 569 AATGAACCTCTTGGGGCCATCGAGATCAAGCATGTATTTGTTGATTTTTCGAAATCT 628
Qy 340 AlaGlyGlnThrLeuAspArgAsnValAla-----GluThrAsnAspVal 355
Db 629 AAGAGTACCTGCTGATATTCATGTAATGATGACGCTTATCTTACCAACCGGATGACA 688
Qy 356 GlyAspGlu 358
Db 689 GTTGATGAA 697
RESULT 4
BE216983 848 bp mRNA linear EST 03-JUL-2000
LOCUS
DEFINITION EST0376 Triticum aestivum lambda zap Triticum aestivum cDNA clone

[illegible]

QY		303 PhegliaValAlaIealSerAspAlaGlyLeuEuglnAlaProValGIThrSerasnLeu	322
Dd		419 TTCTGTGCACGTCGGCTCCGACTCCGTCRACCTCGCCGCCGCTTCCACCAGGAGGTTCC	478
QY		323 TyrlleuaValAlaGlauArgTyrgluilellelaspPherthrAsnPhelaaglyGln	342
Dd		479 TTGCTGGCGCGTGATCGCGGATGTTCATCGACTTCGCGGGGCCAAGCAGCAC	538
QY		343 ThrlleuaspleuAArgasValAlaagluthrAsnspValglyAsppluasgclutyrAla	362
Dd		559 GCGGGACCCCTCGCGGTCCGACGCCGCCGCCGACCCCAGCCGCCGAGAAAGGC	598
QY		363 ArgThrlleuGlualValMetArgPhevalValSerSerylThrValGlualAspAsnserGln	382
Dd		559 CATACGGGGGCCGTATCATACATCGGGGCCGCACTAAC-----	637
QY		383 ValProSerThrLeuarg 388	
Dd		638 ---CCGAGACGACCCGG 652	
RESULT 5			
B0866278			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			

B0866278 739 bp mRNA linear EST 14-AUG-2002
 OGCI13.JV.ab1 OG ABCDI lettuce salinas Lactuca sativa cDNA clone
 OGCI13, mRNA sequence.
 B0866278
 B0866278.1 GI:22251743
 EST.
 Lactuca sativa.
 Lactuca sativa.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
 Lactuca.
 1 (bases 1 to 739)
 Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
 Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison,
 P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
 Church,S., Jackson,L. and Bradford,K.
 Lettuce and Sunflower ESTs from the Compositae Genome Project
 http://compgenomics.ucdavis.edu/
 unpublished (2002)
 Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Asmundson Hall, UCD, Davis, CA 95616, USA
 Tel.: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
 belongs to contig QC_CA_contig2503, see http://cgpdb.ucdavis.edu/
 for details.
 Plate: QGC7 row: I column: 13.
 Location/Qualifiers
 1..739
 /organism="Lactuca sativa"
 /cultivar="Salinas"
 /db_xref="taxon:4236"
 /clone="OGCI13"
 /clone_1fb="OG ABCDI lettuce salinas"
 /lab_host="E.coli"
 /note="Vector: pRCNDASfAD. The library was constructed
 from 10 different sources of RNA from a single genotype.
 Separate cDNAs were generated using primers that
 incorporated unique 5' and 3' tags to distinguish each
 source of RNA. cDNAs were then pooled, size-fractionated,
 directionally cloned into a custom medium-copy vector and
 transformations made with four size classes to minimize
 size bias. Details of each source of RNA and library
 construction can be obtained at http://cgpdb.ucdavis.edu/
 TAG_LIB-OG_ABCDI_lettuce_salinas
 TAG_TISSUE-chemical_induction
 TAG_SEQ-TGTAGCCGGC"
 204 a 167 c 163 g 203 t 2 others

ORIGIN

Alignment Scores:
Pred. No.: 6 64e-20 Length: 739
Score: 293.50 Matches: 75
Percent Similarity: 53.18% Conservative: 42
Best Local Similarity: 34.09% Mismatches: 86
Query Match: 9.20% Indels: 17
DB: 14 Gaps: 6

US-10-080-233-2 (1-594) x BQ866278 (1-739)

QY 184 LeuTPRTHIsAspHisAlaPheMetLysThAlaGluAsnAlaTyrPheGlyGlnAla 203
|||||
5 TTGTTTACACGATCAGCCATGAGGGTTGACAGATCACTTCTTGACAGGTTGTC 64
QY 204 GlyAlaTyrIleIle---AsnAspGluAlaGluAspAlaLeuGlyLeuProSerGlyTyr 222
|||||
65 GGAGCATACATCATCCGTCATCAGACGTTGAATCCCACTCGTTTACCCTCCGCCG--- 121
QY 223 GlyGluPheAspIleProLeuIleLeuThAlaLysTyrTyrAsnAlaAspGlyThrLeu 242
|||||
122 GATGAATTGATGGCCGTTGGTTGTTTCGACCGGAGCTTGAACCTAACGATCCCTT 181
QY 243 ---ArgSerThrGluGlyAspGlnAspLeu-----Trp 253
|||||
182 TACATGGATCCCAACCGAACAACAGATATACACCTCAGTGCAGCGGAGTATTTTC 241
QY 254 GlyAspValIleHisValAsnGlyGlnProTyrProPheLeuAsnValGlnProArgLys 273
|||||
242 GGGGATGCGCATGTTGTTCAACGGAAGAACATGAGTGTGATGATGTTCCGCGAGAAA 301
QY 274 TyrArgPheArgPhePheAsnAlaAlaValSerArgAlaTyrLeuLeuValArg 293
|||||
302 TACCGTTTGTGATCATCAACGCTAGTAAAGCTGTTTAAAGTCTTTTC----- 355
QY 294 ThrSerProAsnValArgIleProPheGlnValIleAlaSerAspAlaGlyLeuLeu 313
|||||
356 -----AGCAACGTTTGAAG-----TTCATCCAGTGGATCTGACTAGCTATAGC 403
QY 314 GlnAlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGluArgTyrGluIleIle 333
|||||
404 GAACATCAGTATACCAACAAAGAGATACCTCTGGCCCACTGAGATAGCTGACGGGTT 453
QY 334 IleAspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaGluThrAsn 353
|||||
464 GTTGACTTTTCAAGACGCAAAATCAAAATTCGTTATTATTACAAAACGGGGCGCTTACCA 523
QY 354 AspValGlyAspGluAspGluTyrAlaArgThrLeuGluValMetArgPheValIleSer 373
|||||
524 TACCCGGGTGAGAGACCGGTCATGATGATCCACGGAAGGTCATGAATTCGTCATCAAT 583
QY 374 SerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspValProPhePro 393
|||||
584 AGTAAACGTGATGTTGATTCATCGAGGTTCTTAAATTAATTAATATATCCGATGCCA 643

RESULT 6

BM143324 592 bp mRNA linear EST 29-NOV-2001
LOCUS BM143324
DEFINITION Gm-c1072-2563 5' similar to TR:023123 023123 F1910.5 PROTEIN. ;
mRNA sequence.
ACCESSION BM143324
VERSION BM143324.1 GI:17153391
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 592)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna

TITLE
JOURNAL
COMMENT

A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyle,T., Underwood,K., Stepien,M., Theising,B., Allen,M., Bowers
Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schuk
R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., Mccann
R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available through: Resgen, Invitrogen Corp, 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: c@resgen.com web site:
www.resgen.com
Seq primer: -40RP from G1bco
High quality sequence stop: 423.
location/Qualifiers

FEATURES
source

1.592
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1072-2563"
/clone_1ib="Gm-c1072"
/rissue_type="seedlings induced for symptoms of SDS
(Sudden Death Syndrome) disease"
/dev_stage="2-3 weeks old"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site:1: EcoRI; Site:2:
XhoI; The cDNA library was constructed from mRNA isolated
from 2-3 week old seedlings that were induced for symptoms
of SDS (Sudden Death Syndrome) disease by the
translocation of culture filtrate of Fusarium solani f.
sp. glycines (Plant Cell Report 18:375-380). Cultivar PI
567374 is partially resistant to the disease SDS. Plant
tissue (expanded leaves, folded leaves, and new shoots)
were collected at 1, 6, 24, and 48 hrs. after inoculation
and their mRNA pooled equally for cDNA construction. The
library was prepared using the Stratagene pBluescript II
SK(+) library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with an XhoI restriction site. EcoRI
adaptors were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA insert is protected
from XhoI digestion via methylation during first strand
synthesis. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
E. coli Electromax DH10B host cells. Plants were inoculated
by Shuxian Li (Glen Hartman lab, University of Illinois).
Library was constructed by Steve Clough (Lila Vodkin lab,
University of Illinois)."
BASE COUNT 155 a 177 c 136 g 124 t
ORIGIN

Alignment Scores:

Pred. No.: 9.47e-20 Length: 592
Score: 290.50 Matches: 69
Percent Similarity: 53.72% Conservative: 32
Best Local Similarity: 36.70% Mismatches: 70
Query Match: 9.11% Indels: 17
DB: 13 Gaps: 5

US-10-080-233-2 (1-594) x BM143324 (1-592)

QY 171 LysAspTyrThrPheProAsnTyrGlnSerAlaArgLeuPheTyrHisAspHisAla 190
|||||
50 AAAGCATATCATCAACCAATATATCAACACGAGGACCTATGGTACCTGACCATGCC 109
QY 191 PheMetLysThrAlaGluAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleIle---Asn 209
|||||

Db 110 ATGGGGTTGACCCGAGTCAACCTTCTAGCTGCTCTGCGAGCCTACATCATTCGCCAC 169
Qy 210 ASpgluAlaGluAspAlaLeuGlyLeuProSerGlyTyrGlyGluPheAspIleProLeu 229
Db 170 CCTCAGATCGAGGAGCCCGCTAGGCTTACCCAGCGT---GAGCATTTGATCGAACGCTG 226
Qy 230 IleLeuThrAlaValSerTyrTyrAsnAlaAspGlyThrLeu---ArgSerThrGluGly 248
Db 227 ATCGTTTCGATCGAGCTTCGACAGCGGTTGATTCATCATAGTTCACCGCGAAC 286
Qy 249 ASP-----GlnAspLeuTyrPglYAspValIleHisValAsn 260
Db 287 AACCTAAATACACCCCTCATAGTGGACGACAGTACTTCGGGAGCCCATCTGTCAC 346
Qy 261 GlyGlnProTyrProPheLeuAsnValGlnProArgLysTyrArgPheArgPheLeuAsn 280
Db 347 GCGAAGGCGTGCGCCGCTCATCGGTCGAGCGTGTAGTATCATGATTCGCGATATCAAC 406
Qy 281 AlaAlaValSerArgAlaTyrPheLeuTyrLeuValArgThrSerSerProAsnValArg 300
Db 407 GCCACACAGCCAGGCTTCTTAGATTCCTTCACCAAC-----GGC 448
Qy 301 IleProPheGlnValIleAlaSerAspAlaGlyLeuGlnAlaProValGlnThrSer 320
Db 449 TTGAGATTCACCCACCGCTGCGATTCGATTCGATTCGAGACCGCATCTGTCAC 508
Qy 321 AsnLeuTyrLeuAlaValAlaGluArgTyrGluIleIleLeuAspPheThrAsnPheAla 340
Db 509 GAGACGCTGTGGGGCCATCTGAGATCACAGACATCGTTGACTTTTCATATCCAG 568
Qy 341 GlyGlnThrLeuAspLeuArgAsn 348
Db 569 AGTAACTTGCTGCTATTCAGCCAC 592

RESULT 7
AF094955/c 1128 bp DNA linear GSS 29-NUG-2000
LOCUS AF094955 Salmonella typhimurium LT2, Lambda DASH II Salmonella
DEFINITION AF094955 typhimurium genomic clone 74-r73, DNA sequence.
ACCESSION AF094955
VERSION AF094955.1 GI:4322797
KEYWORDS GSS.
SOURCE Salmonella typhimurium.
ORGANISM Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
REFERENCE 1 (bases 1 to 1128)
AUTHORS Wong, R.M.Y. and McClelland, M.
TITLE End Sequences of Salmonella typhimurium LT2 Lambda DASHII Clones,
Li-Cor
JOURNAL Unpublished (1999)
CONTACT: McClelland M
Molecular Biology
Sidney Kimmel Cancer Center
3099 Science Park Road, San Diego, CA 92121, USA
Email: mclelland@lifesci.sdsu.edu
Class: Shotgun.
FEATURES
source Location/Qualifiers
1..1128
/organism="Salmonella typhimurium"
/strain="LT2"
/db_xref="taxon:602"
/clone="74-r73"
/clone_lib="Salmonella typhimurium LT2, Lambda DASH II"
/note="Vector: Lambda DASH II; sequenced using Li-Cor
sequencer".

BASE COUNT 260 a 352 c 305 g 211 t
ORIGIN

Alignment Scores: 1.44e-18 Length: 1128
Pred. No.: 283 50 Matches: 96
Score: 38.728 Conservative: 43
Percent Similarity:

Best Local Similarity: 26.74% Mismatches: 127
Query Match: 8.89% Indels: 93
DB: 17 Gaps: 9
US-10-080-233-2 (1-594) x AF094955 (1-1128)

Qy 1 MetLeuPheLysSerThrPglLeuAlaAlaAspGlyLeuLeuSerGlyValLeuGly 20
Db 1066 ATGTCATTCAGTCGCGCTCATGTTCTTCAGCATCG-----GGA 1028
Qy 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40
Db 1027 ATCCGACTATGTGACAGCGGCAATTCCTCCAGAGCG----- 992
Qy 41 ValPheAlaAspSerLeuLeuAlaAlaGlyAspAspAspTyrGlyLysProProTyr 60
Db 991 -----AATCTCCCGCTCAG----- 977
Qy 61 AsnLeuLeuTyrArgAsnAlaLeuProIleProProValLysGlnProLysMetIleIle 80
Db 976 -----CAACACCCGCTGCTGCTCCGCGCTGCGAGTCCCGCTC----- 935
Qy 81 ThrAsnProValThrGlyLysAspIleTyrTyrTyrGluIleGluIleLysProPheGln 100
Db 934 -----GGG 932
Qy 101 GlnArgIleTyrProThrLeuArg-----ProAla 110
Db 931 CAGCGGTGTTTATGAGCTATACAGGACGAGCTGCTTTCAGCAAGGACGCGCGC 872
Qy 111 ThrLeuValGlyTyrAspGlyMetSerProGlyProThrPheAsnValProArgGlyThr 130
Db 871 CCGGCTGTGGAGTGAACGCTGTATATCTGGGGCGACATCCGCTTGGAAGCGCAT 812
Qy 131 GluThrValValArgPheIleAsnAsnAlaThrValGluAsnSerVal----- 146
Db 811 GACGTTAACTCATATACAGACCCGCTGCGGAAATGCTCTCATACGCTGCTGCT 752
Qy 147 -----HisLeuHisGlySerProSerArg-----AlaProPheAspGly 159
Db 751 TTACTGTGTGCGGGCGCGCTGATGGTGGCGCGGTATGATGATGTCGACGCGGAC 692
Qy 160 TrpAlaGluAspValThrPheProGlyLysIleTyrLysAspTyrTyrPheProAsnTyrGln 179
Db 691 TGGGGCGCG-----GCTTTCGCTATTCGTCAG 665
Qy 180 SerAlaArgLeuLeuTyrTyrHisAspHisAlaPheMetLysThrAlaGluAsnAlaTyr 199
Db 664 AGCGCGCGAGCGCTGTGTATCATACGCTAACCGCTAACCGCGCGACAGGTAT 605
Qy 200 PheGlyGlnAlaGlyAlaTyrIleLeuAsnAspGluAlaGluAspAlaLeuGlyLeuPro 219
Db 604 AACGCGCGGACGAGAAATGTGGCTGTGCAACGACATCAATAAACGCTGCCATTCG 545
Qy 220 SerGlyTyrGlyGluPheAspIleProLeuIleLeuThrAlaValTyrTyrAsnAlaAsp 239
Db 544 AACCATTCAGCGCGTGAATTTCCGCTCATTCAGATTAACGCGCGTGAATTCAT 485
Qy 240 GlyThrLeuArgSerThrGluGlyLysAspLysPheLeuTyrPglYAspValIleHisVal 259
Db 484 GGGAGCGCGGAGTACAGGAAACGCGGAGCGGTTCGCGCGATACCTGCTGCTG 425
Qy 260 AsnGlyGlnProTyrProPheLeuAsnValGlnProArgLysTyrArgPheArgPheLeu 279
Db 424 AACGGCGCGCAAGCCCTATGATGAGATGTCGCGGCGTGGGCGGTTCAGTTGTTG 365
Qy 280 AsnAlaAlaValSerArgAlaTyrPheLeuTyrLeuValArgThrSerSerProAsnVal 299
Db 364 AACGCTCGAAGTGTGCGCGCTATCAGTTCAGATGAGCGATGCGCGCGC----- 314
Qy 300 ArgIleProPheGlnValIleAlaSerAspAlaGlyLeuGlnAlaProValGlnThr 319
Db 313 -----CTCATGTGATTCAGGCGATCAGGCGCTTTTAACTGCGCGCTTCGCTC 263

Oy	320	Serpinin	LeuValAlaValAlaGluArgGyrCysIleIleIleIleAaspPheThrAsn	338
Bm519618	111			
LOCUS	262	AAACAGTTGTCACTGGCCCGCCGCCGACGACTGAATTCCTGTTGATTATGACCAC	206	
RESULT 8				
DEFINITION	BMS19618	563 bp	mRNA	linear EST 15-FEB-2002
VERSION	sraB1801.Y1	Gm-cl036	Glycine max cDNA clone SOYBEAN CLONE ID:	
KEYWORDS	Gm-cl036-9433	5'	similar to TR:O23123 O23123 F19610.5 PROTEIN.	:
SOURCE	mRNA sequence.			
ORGANISM	BMS19618	GI:18690770		
	EST.			
	soybean.			
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;			
	Glycine.			
REFERENCE	1	(bases 1 to 563)		
AUTHORS	Shoemaker, R., Kaim, P., Vodkin, L., Expelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person, K., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterson, R. and Wilson, R.			
TITLE	Public Soybean EST Project			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.edu This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: cst@resgen.com web site: www.resgen.com Seq primer: --40RP from GIBCO High quality sequence stop: 433. Location/Qualifiers 1..563 /organism="Glycine max" /db_xref="taxon:3847" /clone="SOYBEAN CLONE ID: Gm-cl036-9433" /clone_id="Gm-cl036" /tissue_type="somatic embryos cultured on MSD 20" /lab_host="DH10B" /note="Vector: pSPOR1; Site1: NotI; Site2: SalI; This cDNA library was constructed from mRNA isolated from somatic embryos (age ranging from 2 months to 9 months) cultured on MSD 20. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a NotI restriction site. SalI linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPOR1 vector. The ligated cDNA fragments were transformed into E.coli Electorax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Vodkin by Anu Khanna at the University of Illinois at Urbana-Champaign. e-mail: l-vodkin@uiuc.edu"			
BASE COUNT	141 a	171 c	128 g	123 t
ALIGNMENT SCORES:				
Pred. No.:	1	95e-18	Length:	563
Score:	277.50	Matches:	67	
Percent Similarity:	53.72%	Conservative:	34	
Best Local Similarity:	53.64%	Mismatches:	70	

Query Match:	8.70%	Indels:	17
DB:	13	Gaps:	5
US-10-080-233-2 (1-594) x BM519618 (1-563)			
QY	174 TyrPheProAsnTyrGlnSerAlaArgLeuLeuTrrTyrHisAspHisAlaPheMetLys	193	
Db	3 CACTACCCAAATATATCAACACACCGGAGAACTATGTATGCATGACCATGCGCATGGGGTTG	62	
QY	194 ThrAlaGlnAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleIle---AsnAspGlnAla	212	
Db	63 ACCCGAGCTCAACCTTCTAGCTGGCTACTCGAGGCTTACATCATTCATTCGGCACCTTAGATC	122	
QY	213 GlnAspAlaLeuGlyLeuProSerGlyTyrGlyGlnPheAspIleProLeuIleLeuThr	232	
Db	123 GAGACACCGCGCTAGCGCTTACCACGGGT---GACAATTCGATCGAACGCTGATCGTGTTC	179	
QY	233 AlaLysTyrTyrAsnAlaAspGlyThrLeu---ArgSerThrGlnGlyLysP---	249	
Db	180 GATCGCAGCTTCCCGCAGGAGCGGTTCGATTCATGAGCTTCACCGGAGACAACTTAA	239	
QY	250 -----GlnAspLeuTyrAspValIleHisValAsnGlyLysPro	263	
Db	240 ATACACCCCTCAGTGGCACCGACGAGTACTGGCGCGACGCCATTCATTGTATACGGCAAGCG	299	
QY	264 TrpProPheLeuAsnValGlnProArgLysTyrArgPheArgPheLeuAsnAlaVal	283	
Db	300 TGCCCGCGGCTCACAGTGGCAGCGTGAATGATGATTCGCGATATACACCGCAGCAAC	359	
QY	284 SerArgAlaTrpLeuLeuTyrLeuValArgThrSerSerProAsnValArgIleProPhe	303	
Db	360 GCCAGGTCCTTACATTCCTTCCACCAAC-----GGCTTGAGATTC	401	
QY	304 GlnAlaIleAlaSerAspAlaGlyLeuGlnAlaProValGlnThrSerAsnLeuTyr	323	
Db	402 ACCCAGCTGCATCGATCGCTGCGCTTACATCGAGAAAGCCGTAAGCAGCACAATGAGACGCTG	461	
QY	324 LeuAlaValAlaGlnArgTyrGlnIleIleIleAspPheThrAsnPheAlaGlyLysThr	343	
Db	462 GTGGGGCCATCGATCAGACATCCAGACATCGTTGTTGACTTTTCATCCAGAGTAACCTTG	521	
QY	344 LeuAspLeuArgAsnValAlaGlu	351	
Db	522 GCTATTCTAGCCACGATGCAAA	545	
RESULT 9			
LOCUS	BG526127		
DEFINITION	56-88 Stevia field grown leaf cDNA Stevia rebaudiana cDNA 5', mRNA		
ACCESSION	BG526127		
VERSION	BG526127.1		
KEYWORDS	EST.		
SOURCE	Stevia rebaudiana.		
ORGANISM	Stevia rebaudiana.		
REFERENCE	Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; eustersids II; Asterales; Asteraceae; Asteroideae; Helianthaceae; Stevia.		
AUTHORS	1 (bases 1 to 766)		
TITLE	Brandle, J.E., Richman, A., Swanson, A.K. and Chapman, B.P.		
JOURNAL	Leaf ESTs from Stevia rebaudiana: A resource for gene discovery in diterpene synthesis		
COMMENT	Unpublished (2001)		
FEATURES	Contact: Jim Brandle Genomics and Biotechnology Agriculture and Agri-Food Canada - SCPPFC 1391 Sandford St., London, Ontario, CANADA, N5V 4R3 Tel: 519 457 1470 Fax: 519 457 3997 Email: jbrandle@eem.agr.ca Seq primer: T3 promoter primer. Location/Qualifiers		

source

1. 766
/organism="Stevia rebaudiana"
/strain="751/1501"
/cultivar="Landrace"
/db_xref="taxon:55670"
/clone_lib="Stevia field grown leaf cDNA"
/tissue_type="leaf"
/dev_stage="field grown, mid-size"
/lab_host="E. coli strain XL0LR"
/note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from polyA+ enriched mRNA from field grown leaves. Mid-size actively growing leaves were collected and pooled from several plants and frozen immediately after harvesting in liquid nitrogen. The cDNA was prepared using an xhoi-poly(dT) linker-primer. An EcoRI adapter was ligated to the blunt end cDNA and the products were digested with EcoRI and xhoi enabling directional cloning into the lambda Zap Express vector. The library was amplified using the host strain XL1-Blue MRF+. Mass excision of the library was performed to obtain pBK-CMV phagemid clones in the host strain XL0LR. Single pass DNA sequencing was performed using the T3 promoter primer: 5' ATTAACCTCCTCAATAAGGA 3'. This library was constructed by Alex Richman."

BASE COUNT 203 a 192 c 174 g 191 t 6 others

ORIGIN

Alignment Scores:
Pred. No.: 4.84e-16 Length: 766
Score: 256.50 Matches: 83
Percent Similarity: 48.668 Conservative: 44
Best Local Similarity: 31.808 Mismatches: 109
Query Match: 8.048 Indels: 26
DB: 12 Gaps: 8

US-10-080-233-2 (1-594) x BG526127 (1-766)

OY 145 SerValHisLeuHISgLySerProSerArgAlaProPheAspGlyTyrPalaGluAspVal 164
::: ||| |||||||
7 GCAACCCACACTCGGTGTTCAACCGCGGTTAAG-----AAGCGGACCCC 54
165 ThrPheProGlyGlyTyrAspPyrTyrPheProAsnTyrGlnSerAlaArgLeu 184
||| ||| |||||||
55 ACTGGACCAAA-ANGNCTTACGATCAAC-----AACCAACAACACCGCGCAACTT 107
185 TrrPyrHisAspHisAlaPheMetLysThrAlaGluAsnAlaTyrPheGlyGlnAlaGly 204
::: ||| |||||||
108 TATTACCATGATCAACGCCATGGGTTGACAGGCGTCAACCTTTCGACGTTTGTTCGGA 167
205 AlaTyrIleIle---AsnAspGluAlaGluAspAlaLeuGlyLeuProSerGlyTyrGly 223
||| ||| |||
168 GCTTACATCATACGACGATCGATGTCGAAACCCGACCTCGGCTCCCTCTGGT---GAT 224
224 GluPheAspIleProLeuIleLeuThrAlaLysTyrTyrAsnAlaAspGlyThrLeu--- 242
||||| ||| |||
225 GAGTTTGAATCGCGCGTGTGTTGATTCGACGCTTCGAAACAATGATCATATATAC 284
OY 243 ArgSerThrGlyGlyGluAspGlnAspLeu-----TrrPgly 254
||| ||| |||
285 ATGCACTACTGTTGAAACCAACCAACATACACCGACGTCGCGACGAGATATTTTGGT 344
OY 255 AspValIleHisValAsnGlyGlnProTrrPheLeuAsnValGlnProArgLysTyr 274
||||| ||| |||
345 GACGTCATTTGTCGAAACGCAAGCATGCTCATGACGCTTCGCGCAAGAAATATAC 404
OY 275 ArgPheArgPheLeuAsnAlaAlaValSerArgAlaTrrPheLeuTyrLeuValArgThr 294
||||| ||| |||
405 CGGTTCCGATATCATACACCAAGTAAAGGTTTTCACACTCTTTTTC----- 455
OY 295 SerSerProAsnValArgIleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGln 314
||| ||| |||
456 ---AGCAATAGGTCTAAGS-----TTTATCCACGCGGATCTGATTCGTCTATATAGTAG 506

OY 315 AlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGluArgTyrGluIleIle-11 334
||| |||
507 CAATCGATATTGTGAAGAGATATCTAGAGCCCATGAAATAGTTGACGTGTCGCT 566
OY 334 eAspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaGluThrAsnAs 354
:|||||: |||
567 TGACTTTCCGAGTCAAAAGTCAAAATTCGTTATCTACGAATGGGCTGATATCATCA 626
OY 354 PValGlyAspGluAspGlyTyrAlaArgThr-LeuGluValMetArgPheValValSer 374
||| |||
627 CCCCGGTGAGATCCGGTTACAGAGACCGCGTAAAGTCAATGATGATCATCATCAAC 686
OY 374 ergLyThrValGluAspAsnSerGlnValProSerThrLeuArgAspValProPhePro 393
||| |||
687 ATCACCAGAGTTGATACCCGACGCGGTTCCGAAAGGCGTTTACAAATACCAACAC 745

RESULT 10
BG053739/c 465 bp mRNA linear EST 25-JAN-2001
LOCUS RH122.9_B08.D1_A003 Rhizome2 (RH122) Sorghum propinquum cDNA, mRNA
DEFINITION
ACCESSION BG053739 GI:12509741
VERSION BG053739.1 GI:12509741
KEYWORDS EST.
SOURCE Sorghum propinquum.
ORGANISM Sorghum propinquum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Sorghum.
1 (bases 1 to 465)
Cordonier-Pratt,M.-M., Gingle,A., Paterson,A., Sudman,M. and Pratt,L.H.
TITLE An EST database from Sorghum: Sorghum propinquum rhizomes
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Seq primer: JEN REV
High quality sequence stop: 421
POLYA-NO.

FEATURES
source
location/Qualifiers
1..465
/organism="Sorghum propinquum"
/db_xref="taxon:132711"
/clone_lib="Rhizome2 (RH122)"
/note="Organ: Rhizomes; Vector: plusescript II from Lambda Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda zap II. Clones to be sequenced were prepared by mass excision."

BASE COUNT 72 a 128 c 193 g 72 t

ORIGIN

Alignment Scores:
Pred. No.: 2.88e-14 Length: 465
Score: 236.00 Matches: 57
Percent Similarity: 53.558 Conservative: 26
Best Local Similarity: 36.778 Mismatches: 54
Query Match: 7.408 Indels: 18
DB: 12 Gaps: 5

US-10-080-233-2 (1-594) x BG053739 (1-465)

OY 173 TyrTyrPheProAsnTyrGlnSerAlaArgLeuLeuTrrPyrHisAspHisAlaPheMet 192
||| ||| |||
452 TACCGGTACCCCAACGTCACCGCGGCAACCTGTGTACACAGACGACGCGCTCGGC 393
OY 193 LysThrAlaGluAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleIle---AsnAspGlu 211
||| ||| |||
392 CTCACCGCGGCCAACCTCTCTCGCGGCTCTCTGCGCTTACATCATCAAGACCGGAG 333

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